

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:33:26 ; Search time 49 seconds
(without alignments)
732.270 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVPGQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

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6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	434	2	US-09-985-689A-1
2	2247	100.0	640	2	US-09-509-814A-6
3	2247	100.0	640	2	US-09-920-954-6
4	2242	99.8	640	2	US-09-509-814A-8
5	2242	99.8	640	2	US-09-920-954-8
6	2191	97.5	434	2	US-09-985-689A-2
7	2183	97.2	639	2	US-09-509-814A-4
8	2183	97.2	639	2	US-09-920-954-4
9	2155	95.9	639	2	US-09-509-814A-1
10	2155	95.9	639	2	US-09-920-954-1
11	2155	95.9	640	2	US-09-509-814A-2
12	2155	95.9	640	2	US-09-920-954-2
13	2143	95.4	434	2	US-09-985-689A-6
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17	1998.5	88.8	433	2	US-09-985-689A-3
18	1987.5	88.5	433	2	US-09-985-689A-4
19	1986.5	88.4	433	2	US-09-104-623A-4
20	1986.5	88.4	433	2	US-09-019-532-4
21	1986.5	88.4	433	2	US-09-338-746-4
22	1986.5	88.4	433	1	US-08-873-479-43
23	1581.5	70.4	345	2	US-09-512-251A-10
24	1581.5	70.4	345	2	US-09-515-150A-10
25	1581.5	70.4	345	2	US-09-136-481-13
26	1581.5	70.4	345	2	US-10-336-324-10
27	452.5	20.1	659	2	US-08-894-818B-1
28	452.5	20.1	659	2	US-09-445-472-12
29	452.5	20.1	659	2	US-10-090-624-12
30	452.5	20.1	659	2	US-09-841-553-1
31	414	18.4	412	2	US-09-445-472-1
32	414	18.4	412	2	US-10-090-624-1
33	414	18.4	522	2	US-08-894-818B-3
34	414	18.4	522	2	US-09-445-472-4
35	414	18.4	522	2	US-10-090-624-4
36	414	18.4	522	2	US-09-841-553-3
37	414	18.4	654	2	US-08-894-818B-35
38	414	18.4	654	2	US-09-445-472-16
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41	401	17.8	659	2	US-08-894-818B-5
42	401	17.8	659	2	US-09-841-553-5
43	346	15.4	520	2	US-09-000-016-7
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45	346	15.4	734	2	US-09-000-016-4
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47	346	15.4	823	2	US-09-000-016-2
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49	304.5	13.6	903	1	US-08-750-532-1
50	304.5	13.6	1398	1	US-08-750-532-9
51	304.5	13.6	1398	2	US-08-894-818B-8
52	304.5	13.6	1398	2	US-09-445-472-6
53	304.5	13.6	1398	2	US-10-090-624-6
54	304.5	13.6	1398	2	US-09-841-553-8
55	295.5	13.2	237	1	US-08-750-532-18
56	283.5	12.6	418	1	US-08-873-479-44
57	276	12.3	418	2	US-09-966-921A-2
58	256.5	11.4	397	2	US-09-328-352-7533
59	254.5	11.3	275	1	US-08-431-387-1
60	251	11.2	280	1	US-08-434-255-8
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65	251	11.2	280	2	US-09-104-623A-2
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67	251	11.2	280	2	US-09-417-359A-2
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69	251	11.2	280	2	US-09-338-746-2
70	251	11.2	370	1	US-08-459-967-6
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72	251	11.2	370	1	US-08-459-871-6
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74	251	11.2	397	1	US-08-434-255-4
75	251	11.2	397	1	US-08-459-967-2
76	251	11.2	397	1	US-08-459-967-4
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78	251	11.2	397	1	US-08-460-327-2
79	251	11.2	397	1	US-08-460-327-4
80	251	11.2	397	1	US-08-459-871-2
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82	251	11.2	397	1	US-09-779-334A-5
83	249	11.1	269	1	US-08-566-369-11
84	249	11.1	269	4	PCT-US95-01937-11
85	249	11.1	269	2	US-09-533-480C-2
86	248	11.0	269	2	US-08-314-309A-6
87	246.5	11.0	402	1	US-08-314-309A-4
88	246.5	11.0	441	1	US-08-566-369-14
89	246	10.9	269	2	US-08-566-369-14
90	246	10.9	269	2	US-09-074-331-14
91	246	10.9	269	4	PCT-US95-01937-14
92	246	10.9	271	2	US-10-242-549-56
93	245	10.9	269	1	US-07-706-691G-4
94	245	10.9	269	1	US-08-254-021-4
95	245	10.9	269	1	US-08-618-446-4
96	245	10.9	269	2	US-08-980-135-4
97	245	10.9	269	2	US-08-585-798-4
98	245	10.9	272	2	US-09-500-135C-236
99	245	10.9	272	2	US-09-768-080-236
100	245	10.9	272	2	US-09-677-822A-236

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ALIGNMENTS

RESULT 1

US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.9e-176;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRKGI TALTALVGRTN 60
Db 1 NDVARGIVKADVQSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRKGI TALTALVGRTN 60

Qy 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120

Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMA PGTFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMA PGTFILSARSSLAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300

Qy 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTQKATYSFTATAGKPLKISLWMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTQKATYSFTATAGKPLKISLWMSDAPASTTA 360

Qy 361 SVTLVNDLVLVTAPNGTQYVGNDFTSYNDWGRNNVNFVINAPOS GTTYTIEVQAYN 420
Db 361 SVTLVNDLVLVTAPNGTQYVGNDFTSYNDWGRNNVNFVINAPOS GTTYTIEVQAYN 420

Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2

US-09-509-814A-6

; Sequence 6, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JF98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-6

Query Match 100.0%; Score 2247; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.2e-175;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRKGI TALTALVGRTN 60
Db 207 NDVARGIVKADVQSSYGLYGQGI VAVADTGLDTGRNDSMHFAFRKGI TALTALVGRTN 266

Qy 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 267 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326

Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMA PGTFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMA PGTFILSARSSLAPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 506

Qy 301 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTQKATYSFTATAGKPLKISLWMSDAPASTTA 360
Db 507 PNGNQGWGRVTLDKSLNVAAYNNESSLSSTQKATYSFTATAGKPLKISLWMSDAPASTTA 566

Qy 361 SVTLVNDLVLVTAPNGTQYVGNDFTSYNDWGRNNVNFVINAPOS GTTYTIEVQAYN 420
Db 567 SVTLVNDLVLVTAPNGTQYVGNDFTSYNDWGRNNVNFVINAPOS GTTYTIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 3

US-09-920-954-6
; Sequence 6, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI

[illegible]

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; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match          99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3e-175;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNKRGITPKPSLLKALIAAGADIIGLY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNKRGITPKPSLLKALIAAGADIIGLY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVITAPNGTYVGNDDFTSPYNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTYVGNDDFTSPYNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 626

Qy 421 VPVGQPTFSLAIVN 434
Db 627 VPVGQPNFSLAIVN 640

RESULT 6
US-09-985-689A-2
; Sequence 2, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT

; ORGANISM: Bacillus sp.
US-09-985-689A:2

Query Match          97.5%; Score 2191; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 2.7e-171;
Matches 419; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNKRGITPKPSLLKALIAAGADIIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNKRGITPKPSLLKALIAAGADIIGLY 300

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360

Qy 361 SVTLVNDLDLVITAPNGTYVGNDDFTSPYNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 420
Db 361 SVTLVNDLDLVITAPNGTYVGNDDFTSPYNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 420

Qy 421 VPVGQPTFSLAIVN 434
Db 421 VPVGQPNFSLAIVN 434

RESULT 7
US-09-509-814A-4
; Sequence 4, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match          97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;
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Qy	1	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDTRGNDSSMHAEFRGKITALLYALGRTN	60
Db	206	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDTRGNDSSMHAEFRGKITALLYALGRTN	265
Qy	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGGLGGLPSNLQTLFSQAFS	120
Db	266	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGGLGGLPSNLQTLFSQAFS	325
Qy	121	AGARIHTNSWGAANVAGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI	180
Db	326	AGARIHTNSWGAANVAGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI	385
Qy	181	TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSSLAPDSSF	240
Db	386	TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSSLAPDSSF	445
Qy	241	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGAADIGLY	300
Db	446	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALTAGAADIGLY	505
Qy	301	PNGNGGWRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA	360
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Qy	361	SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN	420
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Qy	421	VPVGPQTFSLAIVN	434
Db	626	VPVGPQNFSLAIVN	639
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; Sequence 4, Application US/09920954			
; Patent No. 6759228			
; GENERAL INFORMATION:			
; APPLICANT: TAKAIWA, MIKIO			
; APPLICANT: OKUDA, MITSUYOSHI			
; APPLICANT: SAEKI, KATSUHIISA			
; APPLICANT: KUBOTA, HIROMI			
; APPLICANT: HITOMI, JUN			
; APPLICANT: KAGEYAMA, YASUSHI			
; APPLICANT: SHIKATA, SHITSUM			
; APPLICANT: NOMURA, MASAFUMI			
; TITLE OF INVENTION: ALKALINE PROTEASE			
; FILE REFERENCE: 0327-0832-0PCT			
; CURRENT APPLICATION NUMBER: US/09/920,954			
; PRIOR FILING DATE: 2001-08-03			
; PRIOR APPLICATION NUMBER: 09/509,814			
; PRIOR FILING DATE: 2000-04-06			
; PRIOR APPLICATION NUMBER: PCT/JP98/04528			
; PRIOR FILING DATE: 1998-10-07			
; PRIOR APPLICATION NUMBER: JP 9-274570			
; PRIOR FILING DATE: 1997-06-08			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 4			
; LENGTH: 639			
; TYPE: PRT			
; ORGANISM: Bacillus sp.			
US-09-920-954-4			
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Best Local Similarity 96.3%; Pred. NO. 2.1e-170;			
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;			
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Db	206	NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDTRGNDSSMHAEFRGKITALLYALGRTN	265
Qy	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGGLGGLPSNLQTLFSQAFS	120

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LOCATION: (611)..(611)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (632)..(632)
OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-1

Query Match 95.9%; Score 2155; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDGRNDSMHEAPRGKITALYALGRTN 60
Db 206 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDGRNDSMHEAPRGKITALYALGRTN 265
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Db 266 NANDTNGHGHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 325
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Qy 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDRIKPDVMPAGTFFILSARSSLPDSSSF 240
Db 386 TVGATENLRPSFGSYADNINHVAFSSRGPTKDRIKPDVMPAGTFFILSARSSLPDSSSF 445
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVQALRHFVKNRGITPKPSLLKAALIAAGADIGLY 300
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Qy 301 PNGNQWGRVTLDKSLNAVYNESSSLSTSKATYSTATAGKPKISLVMSDAPASTTA 360
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Db 566 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNMDGRNNVNFVFNAPQSGTYYTIEVQAYN 625
Qy 421 VPVGPQTFFSLAIVN 434
Db 626 VPVGPQTFFSLAIVN 639

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RESULT 10
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; Sequence 1, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
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; ORGANISM: Bacillus sp.
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US-09-920-954-1

Query Match 95.9%; Score 2155; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
DB 206 NDVARGIVKADVQSSVGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTNGKGMAPQANLVFQSIMDSGGGLGGLPSNLTTLFSQAYS 120
DB 266 NANDTNGHGHVAGSVLGNSTNGKGMAPQANLVFQSIMDSGGGLGGLPSNLTTLFSQAYS 325
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGTISAPGTAKNAI 180
DB 326 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGTISAPGTAKNAI 385
QY 181 TVGATENLRPFSGVADNINVAQFSRSGPTKGRIKPDVMAFGFILSARSSILAPDSSF 240
DB 386 TVGATENLRPFSGVADNINVAQFSRSGPTKGRIKPDVMAFGFILSARSSILAPDSSF 445
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DB 506 PNGNGQWRVTLDKSLNVAYNNESSLSTSQKATYFTATAGKPKIKSLVMSDAPASTTA 565
QY 361 SVTLVNDLVLVTAPNGTYGVGNDFTSPVNDMNDGRNNVNFVINAPOSQGTITIEVQAYN 420
DB 566 SVTLVNDLVLVTAPNGTYGVGNDFTSPVNDMNDGRNNVNFVINAPOSQGTITIEVQAYN 625
QY 421 VPVGPQTFFSLAVN 434
DB 626 VPVGPQXFFSLAVN 639

RESULT 11
US-09-509-814A-2
; Sequence 2, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUO
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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OTHER INFORMATION: Xaa is any amino acid

Query Match 95.9%; Score 2155; DB 2; Length 640;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAOSSGLYCGOIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 207 NDVARGIVKADVAOSSGLYCGOIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 266
Qy 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIMDSXGGLGGLPSNLQTLFSQAYS 120

Db 267 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIMDSXGGLGGLPSNLQTLFSQAXS 326
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Db 327 AGARIHTNSWGAAVNGAYTTTDSRNVDYVRKNDMTILFAAGNEXPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSSSLAPDSSF 446
Qy 241 WANHDSKIAYMGGTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALTAGAADIGLY 300
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Qy 421 VPVGPQTFSLAIVN 434
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RESULT 12
US-09-920-954-2
Sequence 2, Application US/09920954
Patent No. 6759228
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHIISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/920,954
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/509,814
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 640
TYPE: PRT
ORGANISM: Bacillus sp.
FEATURE:
NAME/KEY: misc feature
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OTHER INFORMATION: Xaa is any amino acid
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; NAME/KEY: misc_feature
; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
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; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (149)..(149)
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; LOCATION: (173)..(173)
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; OTHER INFORMATION: Xaa is any amino acid
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; LOCATION: (189)..(189)
; OTHER INFORMATION: Xaa is any amino acid
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; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (307)..(307)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature

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; LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (370)..(370)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (532)..(532)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (542)..(542)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (585)..(585)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (592)..(592)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (593)..(593)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (597)..(597)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (612)..(612)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: (633)..(633)
; OTHER INFORMATION: Xaa is any amino acid
; US-09-920-954-2

Query Match          95.9%; Score 2155; DB 2; Length 640;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGGQIVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 266

Qy 61 NADTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIQSDSGGGLGGLPSNLQTLFQSAYS 120
Db 267 NADTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIQSDSGGGLGGLPSNLQTLFQSAYS 326

Qy 121 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEXPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVNPAGPTFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVNPAGPTXILSARSSLPDSSF 446

Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAAGADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAAGADIGLY 506

Qy 301 PNGNQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWGRVTLDKSLNVAYVNESSLSSTOKATYXFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLVLVITAPNGTQYVGNDFTPYNDNWDGRNNVENVFNAPQSGTYTTEVQAYN 420
Db SVTLVNDLVLVITAPNGTQYVGNDFTPYNDNWDGRNNVENVFNAPQSGTYTTEVQAYN 420

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Db 567 SVTLVNDLVLITAPNGTXYVGNDFXXPXXNMDGRNNVENVFINXPSGTYTIEVQAYN 626

Qy 421 VPVGPOTFSLAIVN 434
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Db 627 VPVGPQXFSLAIVN 640
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RESULT 13
US-09-985-689A-6
; Sequence 6, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-6

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 2,3e-167;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
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Db 1 NDVARGIVKADVAGSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||

Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
|||

Db 61 NANDPNGHGHVAGSVLGN-ATNKGMAPOANLVFQSIMDSGGGLGGLPANLQTLFSOAYS 119
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Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
|||

Db 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180
|||

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIPKPDVMAPGTFTLSARSLAPDSSF 240
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Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIPKPDVMAPGTFTLSARSLAPDSSF 240
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Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGADIGLGY 300
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Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGADIGLGY 300
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Qy 301 PNGNQGWGRVTLDKSLNVAVYNESSLSSTQKATYSFTATAGPKLKSILVMSDAPASTTA 360
|||

Db 301 PNGNQGWGRVTLDKSLNVAFWNETSSLTQKATYSFTAQSGKPLKISLWSDAPASTSA 360
|||

Qy 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDNMDGRNNVENVFINAPQSGTYTIEVQAYN 420
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Db 361 SVTLVNDLVLITAPNGTKYVGNDFTPDYNDNMDGRNNVENVFINAPQSGTYTIEVQAYN 420
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Qy 421 VPVGPOTFSLAIVN 434
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Db 421 VPOGPQAFSLAIVN 434
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RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.6%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 6.2e-166;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVAGSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||

Db 1 NDVARGIVKADVAGSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
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Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSOAYS 120
|||

Db 61 NANDPNGHGHVAGSVLGN-ATNKGMAPOANLVFQSIMDSGGGLGGLPANLQTLFSOAYS 119
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Qy 121 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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Db 120 AGARIHTNSWGAANVGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 179
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Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIPKPDVMAPGTFTLSARSLAPDSSF 240
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Db 180 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIPKPDVMAPGTFTLSARSLAPDSSF 239
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Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGADIGLGY 300
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Db 240 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGADIGLGY 299
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Qy 301 PNGNQGWGRVTLDKSLNVAVYNESSLSSTQKATYSFTATAGPKLKSILVMSDAPASTTA 360
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Db 300 PNGNQGWGRVTLDKSLNVAFWNETSPLSTQKATYSFTAQAGKPLKISLWSDAPGSTTA 359
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Qy 361 SVTLVNDLVLITAPNGTQVGNDFTPSYNDNMDGRNNVENVFINAPQSGTYTIEVQAYN 420
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Db 360 SVTLVNDLVLITAPNGTKYVGNDFTPDYNDNMDGRNNVENVFINAPQSGTYTIEVQAYN 419
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Qy 421 VPVGPOTFSLAIVN 434
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Db 420 VPVGPOTFSLAIVH 433
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RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson


```

; TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
; TITLE OF INVENTION: Having Protease Activity
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,479
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Agrie, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 5251.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-873-479-42

Query Match 94.6%; Score 2125.5; DB 1; Length 641;
Best Local Similarity 93.5%; Pred. No. 1.le-165;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
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QY 61 NANDTNGHGHVAGSVLGNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 269 NANDPNHGHGHVAGSVLGN-ATNKGMAPOANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 327
QY 121 AGARIHTNSWGAIVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
DB 328 AGARIHTNSWGAIVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 387
QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAPTGFIILSARSSLAPDSSF 240
DB 388 TVGATENLRPSFGSVADNINHVAFSSRGPTGDIKPDVMAPTGFIILSARSSLAPDSSF 447
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIGLY 300
DB 448 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADVGLGF 507
QY 301 PNGNQGWGRVTLDKSLINVAYNNESSLSSTQKATYSFTATAGKPLKISLVMSDAPSTTA 360
DB 508 PNGNQGWGRVTLDKSLNVAFNSTPLSTSQKATYSFTAQAGKPLKISLVMSDAPGSTTA 567
QY 361 SVTLVNDLDLVITAPNGTQYVGNDETSPYNDKWDGNNVNFVINAPOSQGTITIEVQAYN 420
DB 568 SVTLVNDLDLVITAPNGIKYVGNDETAPYDNNWDGNNVNFVINAPOSQGTITIEVQAYN 627
QY 421 VPVGPQTFSIAIVN 434
DB 628 VPVSPQTFSIAIVH 641
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Search completed: March 30, 2006, 08:34:48
Job time : 50 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:34:11 ; Search time 166 Seconds
(without alignments)
1092.397 Million cell u

Title: US-10-820-712A-1

Perfect score:

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVGPQTFSLAIYN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs. 417829326 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

Database :

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Database : Published Applications_AA_Main.*
1: /cn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	#	Length	DB	ID	Description
1	2247	100.0	434	3	US-09-985-689A-1		Sequence 1, Appli
2	2247	100.0	434	4	US-10-385-662-2		Sequence 2, Appli
3	2247	100.0	434	4	US-10-456-479-2		Sequence 2, Appli
4	2247	100.0	434	4	US-10-837-566-1		Sequence 1, Appli
5	2247	100.0	434	5	US-10-820-712A-1		Sequence 1, Appli
6	2247	100.0	434	5	US-10-820-714A-1		Sequence 1, Appli
7	2247	100.0	640	3	US-09-920-954-6		Sequence 6, Appli
8	2247	100.0	640	4	US-10-456-479-4		Sequence 4, Appli
9	2247	100.0	640	4	US-10-784-870-6		Sequence 6, Appli
10	2247	100.0	640	5	US-10-820-712A-3		Sequence 3, Appli
11	2247	100.0	640	5	US-10-820-714A-3		Sequence 3, Appli
12	2242	99.8	434	4	US-10-456-479-11		Sequence 11, Appl
13	2242	99.8	434	5	US-10-820-712A-14		Sequence 14, Appl
14	2242	99.8	434	5	US-10-820-714A-15		Sequence 15, Appl
15	2242	99.8	640	3	US-09-920-954-8		Sequence 8, Appli
16	2242	99.8	640	4	US-10-784-870-8		Sequence 8, Appli
17	2191	97.5	434	3	US-09-985-689A-2		Sequence 2, Appli
18	2191	97.5	434	4	US-10-456-479-10		Sequence 10, Appl
19	2191	97.5	434	4	US-10-837-566-2		Sequence 2, Appli
20	2191	97.5	434	5	US-10-820-712A-12		Sequence 12, Appl
21	2191	97.5	434	5	US-10-820-714A-13		Sequence 13, Appl
22	2193	97.2	639	3	US-09-920-954-4		Sequence 4, Appli
23	2193	97.2	639	4	US-10-784-870-4		Sequence 4, Appli
24	2155	95.9	639	3	US-09-920-954-1		Sequence 1, Appli
25	2155	95.9	639	4	US-10-784-870-1		Sequence 1, Appli
26	2155	95.9	640	3	US-09-920-954-2		Sequence 2, Appli
27	2155	95.9	640	4	US-10-784-870-2		Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-985-689A-1

; Sequence 1, Application US/09985689A
; Publication No. US20030022351A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 3; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.6e-171;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAGSSYGLYGQGI	VADTGLD	TGRNDS	SMHEAF	RKGI	TAL	VAL	GR	TN	60
DB	1	NDVARGIVKADVAGSSYGLYGQGI	VADTGLD	TGRNDS	SMHEAF	RKGI	TAL	VAL	GR	TN	60
QY	61	NANDTNGHGT	HVAGSV	LV	LG	ST	NK	GM	A	P	Q
DB	61	NANDTNGHGT	HVAGSV	LV	LG	ST	NK	GM	A	P	Q
QY	121	AGARIHTNS	WGAA	V	NG	A	Y	T	T	D	S
DB	121	AGARIHTNS	WGAA	V	NG	A	Y	T	T	D	S
QY	181	TVGATENLR	PS	FG	S	Y	AD	N	I	N	H
DB	181	TVGATENLR	PS	FG	S	Y	AD	N	I	N	H
QY	241	WANHDSKY	Y	M	G	G	T	S	M	A	T
DB	241	WANHDSKY	Y	M	G	G	T	S	M	A	T
QY	301	PNGNQGW	R	V	T	L	D	K	S	L	N
DB	301	PNGNQGW	R	V	T	L	D	K	S	L	N
QY	361	SVTLVND	L	D	L	V	I	T	A	P	N
DB	361	SVTLVND	L	D	L	V	I	T	A	P	N
QY	421	VPVGP	Q	T	F	S	L	A	I	N	
DB	421	VPVGP	Q	T	F	S	L	A	I	N	

RESULT 2

US-10-385-662-2

; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KOBAYASHI, TOHRU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938USO
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2

Query Match 100.0%; Score 2247; DB 4; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.6e-171;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAGSSYGLYGQGI	VADTGLD	TGRNDS	SMHEAF	RKGI	TAL	VAL	GR	TN	60
DB	1	NDVARGIVKADVAGSSYGLYGQGI	VADTGLD	TGRNDS	SMHEAF	RKGI	TAL	VAL	GR	TN	60
QY	61	NANDTNGHGT	HVAGSV	LV	LG	ST	NK	GM	A	P	Q
DB	61	NANDTNGHGT	HVAGSV	LV	LG	ST	NK	GM	A	P	Q
QY	121	AGARIHTNS	WGAA	V	NG	A	Y	T	T	D	S
DB	121	AGARIHTNS	WGAA	V	NG	A	Y	T	T	D	S
QY	181	TVGATENLR	PS	FG	S	Y	AD	N	I	N	H
DB	181	TVGATENLR	PS	FG	S	Y	AD	N	I	N	H
QY	241	WANHDSKY	Y	M	G	G	T	S	M	A	T
DB	241	WANHDSKY	Y	M	G	G	T	S	M	A	T
QY	301	PNGNQGW	R	V	T	L	D	K	S	L	N
DB	301	PNGNQGW	R	V	T	L	D	K	S	L	N
QY	361	SVTLVND	L	D	L	V	I	T	A	P	N
DB	361	SVTLVND	L	D	L	V	I	T	A	P	N
QY	421	VPVGP	Q	T	F	S	L	A	I	N	
DB	421	VPVGP	Q	T	F	S	L	A	I	N	

RESULT 3

US-10-456-479-2

; Sequence 2, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:

APPLICANT: SATO, TSUYOSHI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: TAKIMURA, YASUSHI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: NOMURA, MASAFUMI
APPLICANT: KOBAYASHI, TOHRU
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 238700US0
CURRENT APPLICATION NUMBER: US/10/456,479
CURRENT FILING DATE: 2003-06-09
PRIOR APPLICATION NUMBER: JP 2002-186387
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: JP 2002-304232
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Qy 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Qy 421 VPVGQPTFSLAIVN 434
Db 421 VPVGQPTFSLAIVN 434

RESULT 4

US-10-837-566-1
Sequence 1, Application US/10837566
Publication No. US20040203129A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHIISA
TITLE OF INVENTION: Alkaline proteases

FILE REFERENCE: 215483US0
CURRENT APPLICATION NUMBER: US/10/837,566
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: US/09/985,689A
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-837-566-1

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Qy 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Qy 421 VPVGQPTFSLAIVN 434
Db 421 VPVGQPTFSLAIVN 434

RESULT 5

US-10-820-712a-1
Sequence 1, Application US/10820712A
Publication No. US20050026804A1
GENERAL INFORMATION:
APPLICANT: KAO CORPORATION
APPLICANT: Okuda, Mitsuyoshi
APPLICANT: Izawa, Yoshifumi
APPLICANT: Kobayashi, Tohru
APPLICANT: Koyama, Shingo
APPLICANT: Sato, Tsuyoshi
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 251701-US0
CURRENT APPLICATION NUMBER: US/10/820,712A
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 2003-106708
PRIOR FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-1

Query Match      100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGP TKDGR IKPDVMA PGTFFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGP TKDGR IKPDVMA PGTFFILSARSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDL DLVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINA PQSGTYTIEVQAYN 420
DB 361 SVTLVNDL DLVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINA PQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 6
US-10-820-714A-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tōhru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-1

Query Match      100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGP TKDGR IKPDVMA PGTFFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGP TKDGR IKPDVMA PGTFFILSARSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNGWGRVTLDKSLNVAAYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDL DLVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINA PQSGTYTIEVQAYN 420
DB 361 SVTLVNDL DLVITAPNGTQYVGNDFTSYNDNDGRNNVNFVINA PQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 7
US-09-920-954-6
; Sequence 6, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match      100.0%; Score 2247; DB 3; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
```

Db 267 NANTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 506
Qy 301 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLDLVTAPNGQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 506
Qy 301 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLDLVTAPNGQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLDLVTAPNGQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 8
US-10-456-479-4
; Sequence 4, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NORIYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-4

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAAOSSYGLYGQGI VAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAAOSSYGLYGQGI VAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 506

Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 506
Qy 301 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLDLVTAPNGQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLDLVTAPNGQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 626
Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 9
US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAAOSSYGLYGQGI VAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAAOSSYGLYGQGI VAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNHNHVAQFSRGPCKDGRKIPDVNAPGTFILSARSSLPDSSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 506

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Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 10
US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTRNDSSMHFAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTRNDSSMHFAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

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RESULT 11
US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820,714A
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTRNDSSMHFAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVQAQSSYGLYGQGIIVAVADTGLDTRNDSSMHFAFRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADININHAQFSSRGPTKDGRIKPDVMAPGTIFILSARSSLPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLGY 506

Qy 301 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGQGWGRVTLDKSLNAVYVNESSLSSTOKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDWNGRNNVNFVINAPOSQGTITIEVOAYN 626

Qy 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI

```



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; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700U0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11

Query Match          99.8%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Db 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Qy 61 NANTNGHGHGTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
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Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Qy 301 PNGNQGRVTLDKSLNVAVYNSSSLSTSOKATYSFTATAGKPKISLVWSDAPASTTA 360
Db 301 PNGNQGRVTLDKSLNVAVYNSSSLSTSOKATYSFTATAGKPKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNVNFVFNAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNVNFVFNAPQSGTYYTIEVQAYN 420
Qy 421 VPVGPOTFSLAIVN 434
Db 421 VPVGPOTFSLAIVN 434

RESULT 13
US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-US0
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-106708
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-15

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Db 1 NDVARGIVKADVAOSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALLYALGRTN 60
Qy 61 NANTNGHGHGTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANTNGHGHGTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPOGTFILSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALITAGAADIGLY 300
Qy 301 PNGNQGRVTLDKSLNVAVYNSSSLSTSOKATYSFTATAGKPKISLVWSDAPASTTA 360
Db 301 PNGNQGRVTLDKSLNVAVYNSSSLSTSOKATYSFTATAGKPKISLVWSDAPASTTA 360
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Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNVNFVFNAPQSGTYYTIEVQAYN 420
Qy 421 VPVGPOTFSLAIVN 434
Db 421 VPVGPOTFSLAIVN 434

RESULT 14
US-10-820-714A-15
; Sequence 15, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match          99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
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Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 420
Qy 421 VPVGPQTFFSLAIVN 434
Db 421 VPVGPQTFFSLAIVN 434
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RESULT 15

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US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGIYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8
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Query Match          99.8%; Score 2242; DB 3; Length 640;
Best Local Similarity 99.8%; Pred. No. 1.5e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
Qy 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSSLAPDSSF 446
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGAADIGLGY 506
Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 566
Qy 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 420
Db 567 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 626
Qy 421 VPVGPQTFFSLAIVN 434
Db 627 VPVGPQTFFSLAIVN 640
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Search completed: March 30, 2006, 08:37:41
Job time : 167 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:35:01 ; Search time 25 Seconds
(without alignments)

528.471 Million cell updates/sec

Title: US-10-820-712a-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVOAYNPVPGQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.5	12.8	802	6	US-10-510-386-2
2	253	11.3	874	6	US-10-510-386-28
3	253	11.3	1047	6	US-10-510-386-200
4	245	10.9	272	7	US-11-020-602-236
5	240	10.7	269	7	US-11-020-602-6
6	235.5	10.5	275	7	US-11-065-943-54
7	235.5	10.5	275	7	US-11-020-602-3
8	231.5	10.3	274	7	US-11-156-062-14
9	230.5	10.3	274	7	US-11-156-062-12
10	230.5	10.3	379	7	US-11-156-062-23
11	229.5	10.2	274	7	US-11-020-602-5
12	226.5	10.1	274	7	US-11-156-062-4
13	226.5	10.1	274	7	US-11-156-062-8
14	225.5	10.0	274	7	US-11-156-062-10
15	225.5	10.0	274	7	US-11-020-602-208
16	224.5	10.0	274	7	US-11-156-062-6
17	223.5	9.9	275	7	US-11-020-602-4
18	221.5	9.9	274	7	US-11-156-062-16
19	221.5	9.9	274	7	US-11-156-062-18
20	220.5	9.8	274	7	US-11-156-062-2
21	219.5	9.8	382	7	US-11-020-602-2
22	209.5	9.3	280	7	US-11-020-602-209
23	205	9.1	1432	6	US-10-510-386-218
24	203	9.0	1647	7	US-11-052-554A-260
25	181	8.1	740	7	US-11-096-568A-24714

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Sequence 341, App
Sequence 42, Appl
Sequence 212, App
Sequence 9, Appli
Sequence 91, Appl
Sequence 809, App
Sequence 32, Appl
Sequence 354, App
Sequence 160, App

99 104 4.6 355 7 US-11-222-451-2 Sequence 2, Appli
100 104 4.6 639 7 US-11-052-554A-165 Sequence 165, App

ALIGNMENTS

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RESULT 1
US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRN
; ORGANISM: Bacillus licheniformis
US-10-510-386-2

Query Match      12.8%; Score 286.5; DB 6; Length 802;
Best Local Similarity 23.0%; Pred. No. 3.9e-13;
Matches 143; Conservative 69; Mismatches 176; Indels 231; Gaps 27;

QY      2 DVARGIVKADVAQSSYGLYGOQIIVAVADTGLDTRND--SSMHEAFROK--ITALYALGR 58
Db      158 DKSAPPICADQAWKS-GYTGKGIKVAVIDTGVDYTHPLDKNNFGPYKGYGVDFVNDYDPQE 216

QY      59 TNNANDTNG---HGHVHAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGLPSHLQTLF 115
Db      217 TPTGDPGRGATDHGHVHAGTAAAGQI-KGVAPEATLLAYRLVLPFGG--SGTTENVIAGI 273

QY      116 SOAYSAGARIHTNSGAAVNGA-YTTDSRNVDVYRKNDMTILFAAGNEGPNGGTISAPG 174
Db      274 EKAVADGAKVMNLGNSLNSPDYATSI--ALDWMAGGVAVTSGNSGPNWTVGSPG 331

QY      175 TAKNAITVGADE-----NLRPSPGS----- 194
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QY      195 -----YADNINH----- 201
Db      392 SGKDKGVKVAVIQGVIPFVDKAENAKNAGAIGAVIYNNATGEIBANVMGMVPTVKLSK 451

QY      202 -----VAQFSSRGPTKD-GRIPKDVMAPGTFILSA 230
Db      452 EGEKLVQIQEGKHSHVFPFKLDKLGETHIASFSRGPVMDTWIMKDPVSPAGVNIYST 511

QY      231 RSSLAPDSSFANHDSK-----YAYMGGTSMATPIVAGNVVAQLREHFVKNRGITP--KPSL 284
Db      512 IPT-----HDPKNPYGSGKGTSMASPHVAGTAAILKQ-----AKPDWTPEQ 554

QY      285 LKAALIAGNADI-----GLQYPNGNQGHVTLDKSLNVAYNVNESS----- 326
Db      555 IKGVLMTAEKLTDENGKPLPNTQAGSIRIMEALKASSIVTPGSHSYGTFLKDKGKQT 614

QY      327 -----LSTSQKA-----TYGFTTAGKPLKISLVMSD-----APASTT---ASVTLVNDL 368
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QY      369 DLIVTAPNGTQVGNDFTSYNNNDMDGRNVE---NVFINAP-----QSGT 411
Db      670 KTKAGTYEGTVIRE-----DGRKVAETPLILLIVKEPDYPRVTSVTVEPGAQQA 719
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QY      412 YTIEVQAYNVVPVGPQTFTSLAI 432
Db      720 YTIE--AY-LPGGAELAFILV 737

RESULT 2
US-10-510-386-28
; Sequence 28, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRN
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

Query Match      11.3%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.2e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;

QY      25 IVAVADTGLDTRNDSSMHEAFROK---TALYALGRITNNANDTNGHGHVHAGSVLG--- 78
Db      447 VIADVTDGVHDLADLS-----GSVKDEGYNVVGRDTADMDNGHGHVHAGSVLGIAAQD 500

QY      79 NGSTNKGMAPQANLVFQSIMDSGGGLGLPSNLQTLFSQAYSAGARIHTNSGAAVNGAY 138
Db      501 NHFSMAGINAYAKTILPVKVLDSG--SGDTQIANGIYYAADHGAKVINLSLG---GPY 554

QY      139 TDSRNVDVYRKNDMTILFAAGNEGPNGGTISAPGAKNAITVGAENLPSFGSYADN 198
Db      555 SRVMEYALKYAASKNVTIVAATGNDGVS--EISYPASSKYTLSTVGCATNNL----- 602

QY      199 INHVAQSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSFANHDSKYAYMGGTSMAT 258
Db      603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTMSGTSMAA 643

QY      259 PIVAGNVVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGL---GYPNGN----- 304
Db      644 PHVAAAAGLL-----LSQNPSLKPKQIASLLTETTADVAFEEQNPDPDYDLIEPAAQI 698

QY      305 -----QWGRVTLDKSLNVAYNVNESSLSQKATYSFTTATAGKPLKI 347
Db      699 PGYDFVSGWRLNVFHAASVPELNKMHVPLNRHTTAVTGTAKSGVTVKI 747

RESULT 3
US-10-510-386-200
; Sequence 200, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
```



```
RESULT 12
US-11-156-062-4
; Sequence 4, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156.062
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-4

Query Match      10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.2e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRNTNANDTN 66
Db 10 LIKADKVQAO-GFKGANVKVAVLDGTGQASHPDLNVVGG-----ASPVAGEAYN-TDGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDS--GGGLGGLPSNLQTLFSQ----- 117
Db 62 GHGTHVAGTVAALDNTTGVGLGAPSVSLYAVKVLNSSGSGSYGIVSGIEWATTNDMDVI 121
Qy 118 AYSAGARIHTNSMCAAVNGAYTTDSNRVDDYVRKNDMTILFAAGNEGPNG--GTISAPGT 175
Db 122 NMSLGGASGSTAMKQAVDNAYA-----RGVVVVAAGNSGSGTNTTIGYPAK 169
Qy 176 AKNAITYGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILLSARSLA 235
Db 170 YDSVIAVGA-----VDSNENRASFSVG-----AELEVMAFGAGVYSTYPT-- 210
Qy 236 PDSSFWANHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 -----NTYATWDGTSMAHPVAGAAAILSKHPNLSASQVRNR 248

RESULT 13
US-11-156-062-8
; Sequence 8, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156.062
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-8

Query Match      10.0%; Score 225.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.6e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRNTNANDTN 66
Db 10 LIKADKVQAO-GFKGANVKVAVLDGTGQASHPDLNVVGG-----ASPVAGEAYN-TDGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDS--GGGLGGLPSNLQTLFSQAYSAGAR 124
Db 62 GHGTHVAGTVAALDNTTGVGLGAPSVSLYAVKVLNSSG--SGSYGIVSGIEWATTNGMD 119
Qy 125 IHTNSWGAANGVNGAYTTDSNRVDDYVRKNDMTILFAAGNEGPNG--GTISAPGTAKNAITV 182
Db 120 VINSLGGA---SGSTAMKQAVDNAYARGVVVVAAGNSGSGTNTTIGYPAKYDSVIIV 176
Qy 183 GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILLSARSLAPDSSFWA 242
Db 177 GA-----VDSNENRASFSVG-----AELEVMAFGAGVYSTYPT----- 210
Qy 243 NHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 ---NTYATWDGTSMAHPVAGAAAILSKHPNLSASQVRNR 248

RESULT 14
US-11-156-062-10
; Sequence 10, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156.062
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-10

Query Match      10.0%; Score 225.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.6e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRNTNANDTN 66
Db 10 LIKADKVQAO-GFKGANVKVAVLDGTGQASHPDLNVVGG-----ASPVAGEAYN-TDGN 61
Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDS--GGGLGGLPSNLQTLFSQAYSAGAR 124
Db 62 GHGTHVAGTVAALDNTTGVGLGAPSVSLYAVKVLNSSG--SGSYGIVSGIEWATTNGMD 119
Qy 125 IHTNSWGAANGVNGAYTTDSNRVDDYVRKNDMTILFAAGNEGPNG--GTISAPGTAKNAITV 182
Db 120 VINSLGGA---SGSTAMKQAVDNAYARGVVVVAAGNSGSGTNTTIGYPAKYDSVIIV 176
Qy 183 GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILLSARSLAPDSSFWA 242
Db 177 GA-----VDSNENRASFSVG-----AELEVMAFGAGVYSTYPT----- 210
Qy 243 NHDSKYAYMGTSMTPIVAGNVA-----QLREHFVKNR 276
Db 211 ---NTYATWDGTSMAHPVAGAAAILSKHPNLSASQVRNR 248
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:29:31 ; Search time 41 Seconds
(without alignments)
1018.490 Million cells

Title: US-10-820-712A-1

Perfect score:

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNVPVGPQTFSLAIVN 434

Scoring table: BLOSUM62

scoring cable: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

FORC-PROCESSING: MINIMUM MATCH 0%
MAXIMUM MATCH 100%

Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*

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Database :      PIK_80:
1:  pir1:*
```

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1: p1r1:
2: p1r2: *
```

```
z: p1r2: *
3: p1r3: *
```

```
3: pir:
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	523.5	23.3	1743	2	T19279	multidrug resistant
2	497	22.1	1905	2	T19267	multidrug resistant
3	347.5	15.5	444	2	B83891	intracellular alk
4	320.5	14.3	442	2	A69587	intracellular alk
5	310.5	13.8	806	2	A41341	pyrolysins EC 3.4
6	302.5	13.5	1398	2	T18159	pyrolysins EC 3.4
7	283	12.6	580	2	S11890	serine proteinase
8	281	12.5	419	1	S25835	subtilisin (EC 3.4
9	280	12.5	799	2	G83753	subtilisin-type pr
10	279.5	12.4	1345	2	T29090	surface layer-asso
11	277	12.3	420	1	S23407	subtilisin (EC 3.4
12	267	11.9	715	2	JC4908	alkaline serine pr
13	263	11.7	1331	2	A72647	probable surface pr
14	259.5	11.5	757	2	C84120	subtilisin-type pr
15	257.5	11.5	513	1	A35742	subtilisin (EC 3.4
16	253.5	11.3	894	2	F69730	cell wall-associat
17	251	11.2	627	2	D75393	serine proteinase,
18	246.5	11.0	402	1	JU0332	alkaline proteinase
19	246.5	11.0	534	1	JS0173	alkaline proteinase
20	243	10.8	519	2	S71451	haloalysin R4 (EC 3
21	242.5	10.8	401	2	I39974	serine proteinase
22	240	10.7	380	2	A49778	high-alkaline seri
23	240	10.7	488	2	A11930	proteinase (import
24	235.5	10.5	382	1	SUBSN	subtilisin (EC 3.4
25	235	10.5	378	2	A33973	high-alkaline seri
26	235	10.5	382	2	I39780	subtilisin (EC 3.4
27	234	10.4	910	2	C69456	subtilisin sendai
28	234	10.4	1374	2	D72593	hypothetical prote
29	232.5	10.3	525	2	G84406	haloalysin (import

ALIGNMENTS

RESULT 1

multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18279
R:Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, June 1996

A:Reference number: Z18855

A:Accession: T18279

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1743 <SHA>

A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:gi399914; P1

C:Genetics:

A:Gene: tagC

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Best Local Similarity 27.9%; Pred. No. 3.5e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

Qy 19 LYGGQIVAVADTGLDTCR---NDS-----SMHEAFRGKITALYALGRTNANDTNGH 68
Db 314 LRGGQILUSIADTGLDGHCHCFSDSKYPIPLNSVNLNHR-KVYYITSTSDSDKVDGH 372

Qy 69 GTHVAGSVLG-----NGSTNGMAPQANLVFQSIMDSGGGLGGL--PSNLQTLFQAY 119
Db 373 GTHICGSAAGTPEDSSVNISSFGLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429

Qy 120 SAGARIHNSWGA---AVNGAYTTDSNRVDYVRKN-DWMTILFAAGNEGPNGGTIS--A 172
Db 430 DAGARVHCDSGSVSGVEGTSGYSDDTASIDDFLTFHPDFILRAAGN---NEQVLSLT 486

Qy 173 PGTAKNATVGCATENLR-----PSFGSYADNI----- 199
Db 487 QSTAKNVITVGAHQTHENYLTGDPNYINYQSSVDINQELICDFDSRYCNVTTAQCCLES 546

Qy 200 -----NHVAQFSRSGPTKDGRIKPDVMAFGTFL 228
Db 547 NATTGLASCCPTLLRKSVIDAANTOPLLYNENNICSFSKGPETHDGRMKPALVAPGEYIT 606

Qy 229 SARSSLA-----PDSSFWANHDSKIAYMGTSMTATPIVAGNVAQLRHF-----F 272
Db 607 SARSGNANTTDQCGDGL-PNTNALLA-ISGTSMTSPFAAAATTLIRQYLVGDGYPTGS1 664

Qy 273 VKNRCITPKPSLLKAALTAGA-----ADTGLGYPNGN-----QGWGRVT 311
Db 665 VESNKLQPTGSLKALMINNAQLNGTFLQITSSITYPSNQVFNFGASLVQVGGAIR 724

Qy 312 LDKSLNVAVNESS-----SLGTSOKATYSFT-- 338
Db 725 MSNHLHVNNNNNNNNKTSIDGITKFDGIGGLDLRLVKNQWKEESLTGQNTSCFYTK 784

Qy 339 -----ATAGKPLK---ISLWSDAPASTASVTLVNDLDLVI-----TAPNGT 378
Db 785 PSSSSSSGNPIPRVATLVMTDPPSYAGAKFNVLNLDLMTIYYRDNGSTIFYSNQGS 844

Qy 379 QYVGNDFTSFYNDWGRNVENVINAPQSGTYTIEVQAYNVPVGPQTES 429
Db 845 SFGL---LAPTQDT---LNNVEGIHNPTEPMTYRFMVAGTNVPMGPQNF 889

RESULT 2

T18267

multidrug resistance protein - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18267

R:Shaulsky, G.; Kuspa, A.; Loomis, W.F.

submitted to the EMBL Data Library, January 1995

A:Description: An MDR transporter/serine protease gene is required for prestalk special;

A:Reference number: Z18850

A:Accession: T18267

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1905 <SHA>

A:Cross-references: UNIPROT:P54683; UNIPARC:UPI000013687C; EMBL:U20432; NID:g664839; PID

C:Genetics:

A:Gene: tagB

Query Match 22.1%; Score 497; DB 2; Length 1905;

Best Local Similarity 28.0%; Pred. No. 1.9e-23;

Matches 162; Conservative 72; Mismatches 162; Indels 182; Gaps 22;

Qy 19 LYGGQIVAVADTGLDTCR---NDS-----SMHEAFRGKITALYALGRTNANDTNGH 68
Db 376 LRGGQILUSIADTGLDGHCHCFSDSKYPIPNQVNNHRKVVT---YITYHDNEDYVNGH 432

Qy 69 GTHVAGSVLGNG-----STNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYSA 121
Db 433 GTHVCGSAAGTPEDSSWAISSFGLATDAKIAFYD-LSSGSSEPTPEDYSQMYKPLYDA 491

Qy 122 GARIHNSWGA---AVNGAYTTDSNRVDYVRK-NDMTILFAAGNEGPNGGTISAPGTA 176
Db 492 GARVHCDSGSVSLQGYGYSDDAGGIDAFLEYEPEFSILRAAGN-NELFASLLAQATA 550

Qy 177 KNAITVGCATENLRPSFGS-----YADNI----- 199
Db 551 KNAITVGAEQTAHVNYVYSDALEYDFSDNANFORPCLFDKKYCNYYTAKCCSEVSNVKG 610

Qy 200 -----NHVAQFSRSGPTKDGRIKPDVMAFGTFLSARSS- 233
Db 611 QLCCPASIKQNASDFTTQPFYNNENMGFSKGPETHDGLKPDIVAPGEYITSAKNG 670

Qy 234 -----LAPDSFWANHDSKIAYMGTSMTATPIVAGNVAQLRHF-----VKNRGI 278
Db 671 ENSTDQCGDGL--PNANGLMSISGTSMTATPLATAATILRQYLVGDGYPTGESVEENKL 728

Qy 279 TPKEPSLLKAALIAAGADIGLY-----PNCNQGWGRVTLDKSLNVA 319
Db 729 LPTGSLKALMINNAQLNGTYFWSASTPNPSNAIFEQINGANLIQMGALRMN---NWL 785

Qy 320 YVNESS-----SLSTSOKAT-----YSFT-----ATAGK 343
Db 786 YVKSNTPTPSRWIGIGGLGNQKATWKEDSLSSGLNKSICYTKPSSSSSGSGGGGT 845

Qy 344 P-LKISLWSDAPASTASVTLVNDLDL-----VITAPN--GTQYVGNDFTSFYND 391
Db 846 PRIVATLVMTDPPSYGAKFNVLNLDLILLNSDDSDIITIGNSGGSLQAGKVAQP--- 902

Qy 392 NWDGRNVENVINAPQSGTYTIEVQAYNVPVGPQTES 429
Db 903 --DTLNNVEGIHNPTEKAMNYKFTIAGTNVPIGPQKFS 938

RESULT 3

B83891

intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: B83891

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B83891

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <STO>

A:Cross-references: UNIPROT:Q9KBJ7; UNIPARC:UPI000000C3D43; GB:AP001513; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: aprX


```
Db 288 SGGTVSGIPANPAEIVNMSLGGGSCSTTMQN-AINGAVSRGT-----TVV 334
Qy 158 PAAGNEGNCGTISAPGTAKNAITVGATEN--LRPFSGYADNINHVAQFSSRGPTKDG 215
Db 335 VAAGNDASNVSG-SIPANCANVIAVAATTSAGAKASNFGTGI----- 377
Qy 216 IKPDVMAPGTFILSARSS--LAPDSSFANHDSKYAYNGGTSMATPIVAGNVAOLREHFV 273
Db 378 ---DVSAPGSSILSTLNSGTTTPGS-----ASYASVNGTSMASPHVAGVVALVQS--V 425
Qy 274 KNRGITPK--PSLLK--AALTAGAADICLGYPNGNGQGRVTLDKSLNVAVVNESS--- 325
Db 426 APTALTPAAVETLLKNTRAPUGAC-----SGCGAGIVNADAAVTAA-INGSGGGG 477
Qy 326 -----SLTSOKATYSFTATAGKPLKISLVMSDAPASTTASVTIL---VND 367
Db 478 GGGNTLNGTPTVGLGAATGAELNYTITVPAG-----SCTLTVTTSGSGSD 523
Qy 368 LDLVI---TAPNGTQYVGNDFTSYNDWNDRGNVNFVINAPOSQGYTIEVQYVNVPG 424
Db 524 ADLYVRAGSAPTDASVT-----CRPYRS-----GNAETCTITAP-SGTYYVRLKAYS--- 569
Qy 425 PQTES 429
Db 570 --TFS 572

RESULT 8
S25835
subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain T441)
C;Species: Bacillus sp.
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C;Accession: S25835
R;Davail, S.; Feller, G.; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillu
A;Reference number: S25835; MUID:93012966; PMID:1398082
A;Accession: S25835
A;Molecule type: DNA
A;Residues: 1-419 <DAV>
A;Cross-references: UNIPARC:UPI00000B877A; EMBL:X63533; NID:g40198; PID:CAA45096.1; PID
C;Superfamily: Subtilisin; subtilisin homology
C;Keywords: extracellular protein; hydrolase; serine proteinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-110/Domain: propeptide #status predicted <PRO>
F;111-419/Product: microbial serine proteinase #status predicted <MAT>
F;135-373/Domain: subtilisin homology <SBT>
F;144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 12.5%; Score 281; DB 1; Length 419;
Best Local Similarity 33.0%; Pred. No. 1.3e-10;
Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;

Qy 21 GQGQIVAVADTGLDTRNDSSMH-EAFRGKITALYALGRT---NNANDTNGHGHVAGSV 76
Db 135 GAGINIAVLDTGVNTNHPDLSNNVEQCKD-----FTVGTNETDNCSTDRQGHGTHVAGSA 189
Qy 77 LGNGSTNK---GMAPOANL-VFQSIMDSGGGLG-GLPSNLQTLFSQAYSAGARLHTN-SW 130
Db 190 LANGGTSGVYGVAPEADLWAKYVLGGDGGGYADDAEATRHAGDQATALNTKVVIMNSL 249
Qy 131 GAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEPGNGGTSAPGTAKNAITVGATENLRP 190
Db 250 GSSGESSILT---NAV DYAYDKGVLLITAAAGNSGPKSGISGYPALVNAVVALENTIQ 306
Qy 191 SFGSYADNINHVAQFSSRGPTKDG-----RIKPDVMAPGTFILSARSSLAPDSSFWANH 244
Db 307 N-GTY-----RVADFSSRGHRTAGDYVIQGDVEIGAPGAAYVST-----W--F 348
Qy 245 DSKYAYMGGTSMATPIVAGNVAOL 268
Db 349 DGGYATISGTSMASPHAGLAAKI 372
```

RESULT 9

G83753

subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: G83753

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira-

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: G83753

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-799 <STO>

A;Cross-references: UNIPROT:O9KEMI; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID

A;Experimental source: strain C-125

C;Genetics:

A;Gene: vpr

C;Superfamily: microbial serine proteinase vpr; subtilisin homology

C;Keywords: hydrolase; serine proteinase

F;1-29/Domain: signal sequence #status predicted <SIG>

Query Match 12.5%; Score 280; DB 2; Length 799;

Best Local Similarity 24.7%; Pred. No. 3.7e-10;

Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;

Qy 18 GLYCGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNANDT-----NGH 68

Db 171 GYTGGITVAILDTGVDTYTHPD--LVHAF-GDYKGMDFIDNDDDPQETPGDPRGIETTH 227

Qy 69 GTHVAGSVLNGSTNKGMAPQANLVFOSIMDSGGGLGGLPSNLQTLFSQAYSAGARLHTN 128

Db 228 GTHVAGTVAANGLI-KGVAPDANLLAVRVLGPGG--RGSTAGVIAGIERAVQDGADIMNL 284

Qy 129 SWGAANVAVTTSRVNDDYVRKNDMTILFAAGNEPGNGGTSIAPGTAKNAITVGATENL 188

Db 285 SLGNTLNDPDPFATSIAL-DWMAEGVVAVTSSNGSPNNWTVGSPGTSRDAISVGAT--- 340

Qy 189 RPSFGSV-----ADINNH----- 201

Db 341 RLPYNTKASVFTSDGIDYPSADIMGFPDSEELLELDGETYEYAFAGLGKPGDFEGVDVE 400

Qy 202 ----- 201

Db 401 GKTALIVRGIPFVEXAENAKAGAVGAILIYNNVAGVQTPVPGIAPTILMSNEDGLKMR 460

Qy 202 -----VAQFSSRGPT-KDGRIPKPDVMAPGTFILSARSSLAPD 237

Db 461 NELENGQNTVTFSTIEFDKLVGETVADPSSRGPMVHTWMIKPDVSPAGVAIVSTIPTHPD 520

Qy 238 SSFWANHDSKYAYMGGTSMATPIVAGNVAOLREHFVKNRGITPKPSLLKAAALIAGADI- 296

Db 521 DPY-----GYGRQGTSMASPHVAGAAALLLEAH-PNWGV----DHVKAALMNTAENLV 569

Qy 297 ---GLGYPNGNGQGRVTLDKSLNVAVVNESSLSSTSQKATY-SFTATAGKPLK 346

Db 570 DENGNYPHNTQAG-----SIRIVDAIESETLVTPGSHSFGTFTKERSQKVE 617

RESULT 10

T29090

surface layer-associated STABLE proteinase - Staphylothermus marinus

N;Alternate names: hyperthermostable proteinase

C;Species: Staphylothermus marinus

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T29090

R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.

Curr. Biol. 6, 739-749, 1996

A;Title: A hyperthermostable protease of the subtilisin family bound to the surface layer

A;Reference number: Z20559; MUID:96385442; PMID:8793300

A;Accession: T29090

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-1345 <MAT>
 A:Cross-references: UNIPROT:Q54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PIDN
 A:Experimental source: strain F1
 C:Function:
 A:Description: probably serves an exodigestive function related to the organism's energy
 A:Note: stoichiometric 8-layer component

Query Match 12.4%; Score 279.5; DB 2; Length 1345;
 Best Local Similarity 29.9%; Pred. No. 7.9e-10;
 Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;

QY 46 PRGKITALYALGRNTNANDTGHGTHVA-----GSLV-----GNGSTNK--GMAPOANLV 93
 DB 445 YQGRYLAL-----VSDFHGHTSVATVIAASGRVLYDYGDKLYRMGVAPGAKI- 495
 QY 94 PQSIMDSGGIGLPLSNLQTLFSQAYSAG-----ARHNTNSW 130
 DB 496 -----AGDADWLLGNLVL--EAWLAGFNIVTEEDGVYVLSLDPPGPHRADIIISNW 546
 QY 131 GAAVNGAYTTDSRNV-----DYVRKNDMTILFAAGNEGPNNGTISAPGTAK 177
 DB 547 GSIYINFLWQPPGIDYRSSEFMDEILAIRNYLIGDHVTIVFAAGNEGPGYSSNGAPGTGL 606
 QY 178 NAITVGATE--NLRPSFG---SYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARS 232
 DB 607 LVITAGASTLDYTRIYGYPEGYAD---EVIPFSRGTGQGYPKPDIVNIGAFEMASTR 663
 QY 233 SLAPDSSFWANHDSKYAVMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIJAG 292
 DB 664 TI-DORGGAQPD---VFGTSEATPYTSGTLALVFQAYKEVYNTTDPDPTAKILLKSS 718
 QY 293 AADIGLYPNQNGQGRVTLQKSLNVAVNE 323
 DB 719 AKDI--WYPAFSQSGRVDALKAADTVFISE 747

RESULT 11
 S23407
 Subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)
 C:Species: Bacillus sp.
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
 C:Accession: S23407
 R:Narinx, E.; Davail, S.; Feller, G.; Gerday, C.
 Biochim. Biophys. Acta 1131, 111-113, 1992
 A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic
 A:Reference number: S23407; MUID:92256481; PMID:1581352
 A:Accession: S23407
 A:Molecule type: DNA
 A:Residues: 1-420 <NAR>
 A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:X62369; NID:g40200; PIDN
 C:Genetics:
 A:Gene: sub1
 C:Superfamily: Subtilisin; subtilisin homology
 C:Keywords: extracellular protein; hydrolase; serine proteinase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-111/Domain: propeptide #status predicted <PRO>
 F:112-420/Product: microbial serine proteinase #status predicted <MAT>
 F:136-374/Domain: subtilisin homology <SBT>
 F:145,185,360/Active site: Asp, His, Ser #status predicted

Query Match 12.3%; Score 277; DB 1; Length 420;
 Best Local Similarity 31.2%; Pred. No. 2.4e-10;
 Matches 98; Conservative 44; Mismatches 120; Indels 52; Gaps 16;

QY 21 GOGQIVAVADTGLDGRNDSSMHEAFRGKITAL--VALGRT--NNANDTNGHGHVAGS 75
 DB 136 GGGINIAVLDTGNTN-----HPDLRNVEOCKDFTVGTNTNSCTDRQGHGHVAGS 189
 QY 76 VLNGSTNK--GMAPOANL--VFQSIMDSGGGLG--GLPSNLOTLSQAYSAGARIHTN-S 129
 DB 190 ALADGGTGVGVAPDADLWAYKVLGDGSGYADIAAAIRHAGDQATALTNTKVVINMS 249

QY 130 WGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGTISAPGTAKNAITVGATENLR 189
 DB 250 LGSSGESSLITNAV---YSYNGVLLIAAAGNSGVPQSGISGYPGALVNAVVAALEN-K 305
 QY 190 PSFGSYADNINHVAQFSRGT-KDG-----RIKPDVMAPTGTFILSARSLAPDSSFWAN 243
 DB 306 VENGTY-----RVADFSRSGYSTDGDYATQKQDVEISAPGAAYST-----W-- 348
 QY 244 HDSKYAVMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAIJAGAADIGLYPNG 303
 DB 349 FDGGYATISGTSWASPHRAAGAAKIWAQYPSASNVVRGELQYRAY---ENDILSGIYAG 405
 QY 304 -----NOQWGRVTL 312
 DB 406 YGDDFASGFGFAIV 419

RESULT 12
 JC4908
 alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
 N:Alternate names: sutilsase
 C:Species: Alteromonas sp.
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
 C:Accession: JC4908
 R:Tsujiibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
 Biosci. Biotechnol. Biochem. 60, 1284-1288, 1996
 A:Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacter
 A:Reference number: JC4908; MUID:97141200; PMID:8987544
 A:Accession: JC4908
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-715 <TSU>
 A:Cross-references: UNIPROT:P70765; UNIPARC:UPI000017A928; DBJ:D38600; NID:gl536787; PII
 A:Experimental source: strain O-7
 C:Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sensit
 C:Genetics:
 A:Gene: aprI
 C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type
 C:Keywords: hydrolase
 F:1-40/Domain: signal sequence #status predicted <SIG>
 F:41-150/Domain: amino-terminal propeptide #status predicted <ATP>
 F:151-496/Product: alkaline serine protease I #status predicted <MAT>
 F:182-452/Domain: subtilisin homology <SBT>
 F:497-715/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:239-294,335-372,478-481/Disulfide bonds: #status predicted

Query Match 11.9%; Score 267; DB 2; Length 715;
 Best Local Similarity 25.9%; Pred. No. 2.1e-09;
 Matches 124; Conservative 51; Mismatches 168; Indels 136; Gaps 23;

QY 21 GOGQIVAVADTG---LDTGRNDSSMHEAFRGKITALYALGRTNNAND-----TNG---- 67
 DB 182 GQGVVAVLDTGYPHPLDLDANILPGYDMISNTFVANDGGARDNDARDPGDAVTRGCGT 241
 QY 68 -----HGTHVAG---SVLNGSTNKGMAPOANLVFQSIMDSGGGLGLP 108
 DB 242 DSSGQVPVPRADQSDSWGHGTHVAGTVAATNNGEGVAGVAYDAKVVPVRL---GKCGGLT 298
 QY 109 SNLQTLFSQAYSAGARIHTNSWGAIV-----NGAYTTDSRNVDDYVRKNDMTILFAAG 161
 DB 299 SDIADGIIWASGGSDRVPANANPAVIVNNSLGGGACSAATTQNAINQARNNGTIVIAAG 358
 QY 162 NEGPNNGTISAPGTAKNAITVGAT--ENLRPSFGSYADNINHVAQFSRGTGDKRIKPD 219
 DB 359 NDNDNSANYN--PGNCNGVNVNVA SVGRGSRAYSYNYGANI-----D 398
 QY 220 VMAPGTFILSARSLAPDSSFWANHDS-----KYAYMGTSMATPIVAGNVAQLR-- 269
 DB 399 VAAFG-----GQASPADDPGEGILSTHNSGSGAPSNDSYHSQGSTWAAPHVAGVAALIKQA 454
 QY 270 -----EHFVKV--RGITPKPSLLKAAIJAGADI--GLG-----YPNGNQGHGRVTL 312
 DB 455 KPSATPDEVEITLKTRTSFAGSCSNCGTGVVDAAAAVNEALGDVVVTPPTGT-----TL 508

Eur. J. Biochem. 173, 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine
A:Reference number: S00620; MUID:88225062; PMID:3286255
A:Accession: S00620
A:Molecule type: DNA
A:Residues: 75-442 <KWO>
A:Cross-references: UNIPARC:UPI0000170448; EMBL:X07734; NID:948069; PIDN:CAA30559.1; PID
A:Note: part of this sequence, including the amino and carboxyl ends of the mature prote
R:Matsumura, H.; Tokugawa, K.; Hamaki, M.; Mizoguchi, H.; Terada, I.; Kwon
Eur. J. Biochem. 171, 441-447, 1988
A:Title: Purification and characterization of aqualysin I (a thermophilic alkaline serin
A:Reference number: S00324; MUID:88151937; PMID:3162211
A:Accession: S00324
A:Molecule type: protein
A:Residues: 128-170 <MATS>
A:Cross-references: UNIPARC:UPI0000172C23
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-127/Domain: propeptide #status predicted <PRO>
F:128-408/Product: aqualysin I #status experimental <MAT>
F:157-364/Domain: subtilisin homology <SBT>
F:255-257,281-283/Region: S1 specificity crevice #status predicted
F:409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F:166,197,349/Active site: Asp, His, Ser #status predicted

Query Match 11.5%; Score 257.5; DB 1; Length 513;
Best Local Similarity 26.0%; Pred. No. 5.4e-09;
Matches 117; Conservative 44; Mismatches 144; Indels 145; Gaps 23;

Qy 16 SYGLYGQGIIVAVADTGLDGTGRNDSSHEAFRGKITALLY-ALGRTNNANDTNGHGHVAG 74
Db 152 TYTATGRGVNVYDITGRT-----THREPGGARVGYDALG--GNGQDCNGHGHVAG 203
Qy 75 SVLGNSTNKGMAPQANLVFQSIIMD--SGGGLGGLPSNLQTLFSQAYSAGARIHTN---- 128
Db 204 TI---GGVTYGVAKAVNLVAVRLDCNGSGSTSGVIAGVDWV-----TRNHRPPAVA 252
Qy 129 --SWGAAVNGAYTTDSRVDDYVRKN---DMTILFAGNEGPNGGTISAPGTAKNAITVG 183
Db 253 NMSLGGGVSTA-----LDNAVKNISIAAGVYVAAAGNDNANACNYS-PARVAEALTVG 304
Qy 184 AT--ENLRPSFGSYADNINHVAFSSRGRTKDGRIKPDVMAPGTFILSARSLAPDSSF 241
Db 305 ATSSDARAFSNVGSV-----DLFAPGASIPSA-----W 335
Qy 242 ANHDSKYAYMGSTMATPIVAGNVAQLREHFVKNRGITP---KPSLLKAALIAGAADIGL 298
Db 336 YTSDTATQTTLNGTSMATPHVAG-VAAL--YLEQNPSATPASVASAILNGATTGRLSGIGS 392
Qy 299 GYPNGNQGWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKISLVNSDAPAST 358
Db 393 GSPN-----RLLYSLLSSGS-----GSTAPCTS 415
Qy 359 ---TASVTLVNDLVLITAPNGTQY-----VGNDFTSPYNDNDGDN--- 397
Db 416 CSYITGSLSGGPDYNF---QNGTYIYSPAGTHRAWLKGPA GTDF-DLYLWRWDGSRWLT 471
Qy 398 -----NVENVFVINAPOSQGTYYIEVQAYN 420
Db 472 VGSSTGPTSEESLSYSGTAGYVYLWRIYAYS 501

Search completed: March 30, 2006, 08:33:55
Job time : 44 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:26:16 ; Search time 228 Seconds
(without alignments)
1342.979 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSGLY.....EVOAYNPVGPQTFLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2247	100.0	640	2	Q93UV9_9BACI
2	2242	99.8	640	2	Q76184_9BACI
3	2183	97.2	639	2	Q9AQR3_9BACI
4	2143	95.4	434	2	Q9AQR0_9BACI
5	1998.5	88.9	433	2	Q9AQR1_9BACI
6	1994.5	88.8	433	2	Q9AQR4_9BACI
7	1987.5	88.5	433	2	Q9AQR2_9BACI
8	870.5	38.7	697	2	Q4NB18_9MICC
9	754.5	33.6	711	2	Q6MKR4_DBEBA
10	739.5	32.9	1748	2	Q4NVB5_GDELTA
11	592	26.3	1088	2	Q4HUV5_GIBZE
12	580	25.8	2030	2	Q747P6_GEOSL
13	531.5	23.7	1741	2	Q54MB4_DICDI
14	523.5	23.3	1743	1	TAGC_DICDI
15	511.5	22.8	1825	2	Q8T9W1_DICDI
16	497	22.1	1905	1	TAGB_DICDI
17	497	22.1	1906	2	Q54MB3_DICDI
18	447	19.9	1752	2	Q9GNT7_DICDI
19	425.5	18.9	1388	2	Q580L9_9TRYP
20	414	18.4	654	2	Q8UOC9_PYRFU
21	414	18.4	663	2	Q5J1Z5_PYRKO
22	406.5	18.1	561	2	Q8RBJ2_THETN
23	398	17.7	1239	2	Q9FBZ4_STRCO
24	381	17.0	430	2	Q8ENV1_OCEIH
25	376	16.7	1253	2	Q9FCO6_STRCO
26	366	16.3	1102	2	P95684_STRAO
27	363.5	16.2	1208	2	Q82BT4_STRAW
28	349	15.5	1245	2	Q9RL54_STRCO
29	347.5	15.5	444	2	Q9KBJ7_BACHD
30	346.5	15.4	1139	2	Q82I39_STRAW
31	346	15.4	1105	2	Q8KKH6_STRVD

32	340	15.1	442	2	Q5L315_GEOKA
33	338	15.0	412	2	Q9AER6_THEYO
34	338	15.0	1237	2	Q8GQT4_STRAZ
35	337	15.0	412	2	Q8RC68_THETN
36	337	15.0	1294	2	Q50HM7_STRSH
37	336	15.0	795	2	Q5NW24_9ARCH
38	332.5	14.8	442	2	Q651P4_BACLD
39	328.5	14.6	1220	2	Q910A0_STRCO
40	327.5	14.6	435	2	Q8EMJ3_OCEIH
41	324.5	14.4	818	2	Q79CG2_BACSP
42	324.5	14.4	824	2	Q45464_BACSP
43	320.5	14.3	442	2	Q31788_BACSU
44	320.5	14.3	891	2	Q93635_THESU
45	310.5	13.8	806	1	SUBV_BACSU
46	308.5	13.7	431	2	Q983L6_BACSH
47	308	13.7	1899	2	Q67RJ0_SYMTH
48	307.5	13.7	646	2	Q52R76_BACSU
49	306.5	13.6	524	2	Q5UEH9_PYRKO
50	306.5	13.6	1398	2	Q9P9L1_PYRWO
51	304.5	13.6	1398	1	PLS_PYRFU
52	297	13.2	1135	2	Q9P9D1_9EURY
53	294.5	13.1	434	2	Q54327_BACSH
54	290	12.9	891	2	Q4H8C2_9DEIO
55	289	12.9	798	2	Q68YD0_9BACI
56	288.5	12.8	808	2	Q6L9U6_9BACI
57	287.5	12.8	798	2	Q68YD2_9BACI
58	286.5	12.8	802	2	Q65DN2_BACLD
59	286	12.7	848	2	Q4HCE6_9DEIO
60	285.5	12.7	808	2	Q6L9U7_9BACI
61	285	12.7	808	2	Q6X5Y8_XANNA
62	285	12.7	798	2	Q68YD1_9BACI
63	283	12.6	416	2	Q6W4N2_9BACI
64	283	12.6	580	1	EXPR_XANCP
65	283	12.6	580	2	Q4URAO_XANCP
66	282.5	12.6	586	2	Q4UT02_XANCP
67	282.5	12.6	586	2	Q6PAL8_XANCP
68	282.5	12.6	807	2	Q6L9U5_9BACI
69	281	12.5	419	2	Q45681_BACSU
70	280.5	12.5	514	2	Q4H6A0_9DEIO
71	280.5	12.5	808	2	Q6L9U8_9BACI
72	280	12.5	799	2	Q9KEM1_BACHD
73	279.5	12.4	1345	2	Q54437_STAMA
74	278.5	12.4	959	2	Q8PMS7_XANAC
75	277.5	12.3	621	2	Q9F486_ALTSO
76	277.5	12.3	621	2	Q53401_9ALTE
77	277.5	12.3	1467	2	Q4X8M2_9BACI
78	277	12.3	420	1	SUBT_BACS9
79	277	12.3	942	2	Q5HIN5_XANOR
80	273.5	12.2	513	2	Q64FJ8_9DEIN
81	272.5	12.1	568	2	Q8PMC0_XANAC
82	272.5	12.1	575	2	Q8PNW1_XANAC
83	271.5	12.1	759	2	Q5WB69_BACSK
84	270	12.1	1101	2	Q82CF0_STRAW
85	268.5	11.9	403	2	Q45463_BACSP
86	268.5	11.9	814	2	Q82VB3_NITEU
87	267.5	11.9	1413	2	Q4MN45_BACEE
88	267	11.9	715	2	P70765_ALTSO
89	265	11.8	1098	2	Q9L1Z8_STRCO
90	265	11.8	1406	2	Q632G9_BACZ
91	265	11.8	1627	2	Q5FIZ3_LACAC
92	264.5	11.8	966	2	Q4USI3_XANCP
93	264.5	11.8	966	2	Q8PB28_XANCP
94	263	11.7	701	2	Q84FM9_FERIS
95	263	11.7	1331	2	Q9VEG9_AERPE
96	263	11.7	1571	2	Q8GCW3_STRAA
97	262.5	11.7	617	2	Q93IQ4_XANNA
98	262.5	11.7	1407	2	Q4MN80_BACCE
99	262	11.7	1407	2	Q816G4_BACCR
100	261	11.6	425	2	Q647R6_9ARCH

ALIGNMENTS

RESULT 1

Q93UV9_9BACI
ID Q93UV9_9BACI PRELIMINARY; PRT; 640 AA.
AC Q93UV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protease.
GN Name=PROF;
OS Bacillus sp. KSM-KP43.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=109322;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KP43;
RA Itoh S., Saeki K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051423; BAB55674.2; -; Genomic_DNA.
DR PDB; 1WMD; X-ray; A=207-640.
DR PDB; 1WME; X-ray; A=207-640.
DR PDB; 1WMF; X-ray; A=207-640.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;

Query Match 100.08; Score 2247; DB 2; Length 640;
Best Local Similarity 100.08; Pred. No. 4.2e-139; Indels 0; Gaps 0;
Matches 434; Conservative 0; Mismatches 0;
QY 1 NDVARGIVKADVAAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 506
QY 301 PNGNGWGRVTLDKSLNVAAYNESSLSSTSKATYSFTATAGKPKIKSLVMSDAPASTTA 360
DB 507 PNGNGWGRVTLDKSLNVAAYNESSLSSTSKATYSFTATAGKPKIKSLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

RESULT 3

Q9AQR3_9BACI
ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
AC Q9AQR3;

RESULT 2

Q76L84_9BACI
ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
AC Q76L84;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protease.
OS Bacillus sp. KSM-9865.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=192495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-9865;
RA Okuda M., Saeki K., Kobayashi T.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
DR HSSP; P00782; IAQN.
DR SMR; Q76L84; 207-640.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;

Query Match 99.88; Score 2242; DB 2; Length 640;
Best Local Similarity 99.88; Pred. No. 9e-139; Indels 0; Gaps 0;
Matches 433; Conservative 1; Mismatches 0;
QY 1 NDVARGIVKADVAAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAAQSSYGLYGQGI VAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 506
QY 301 PNGNGWGRVTLDKSLNVAAYNESSLSSTSKATYSFTATAGKPKIKSLVMSDAPASTTA 360
DB 507 PNGNGWGRVTLDKSLNVAAYNESSLSSTSKATYSFTATAGKPKIKSLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTPYNDNWDGRNNVENVFINAPQSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Name=PROA;
GN Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RA MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; CO:0008233; F:peptidase activity; IEA.
DR GO; CO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;

Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 6.7e-135;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
Db 206 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 265

Qy 61 NANTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 266 NANTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 325

Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEPNGGTTISAPGTAKNAI 180
Db 326 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNERPNGGTTISAPGTAKNAI 385

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAQCTFILSARSSILAPDSSF 240
Db 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAQCTFILSARSSILAPDSSF 445

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 300
Db 446 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADVGLGY 505

Qy 301 PNGQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 506 PNGQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 565

Qy 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 566 SVTLVNDLDLIVITAPNGTRYVGNDFSPAFDNNWDGRNNVENVFINPQSGTYTIEVOAYN 625

Qy 421 VPVGQPTFSLAIVN 434
Db 626 VPVGQPTFSLAIVN 639

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 1.7e-132;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
Db 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60

Qy 61 NANTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNVSTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEPNGGTTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMAVLFAGNEPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAQCTFILSARSSILAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAQCTFILSARSSILAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 300

Qy 301 PNGQGWGRVTLDKSLNVAYVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGQGWGRVTLDKSLNVAFVNETSSLSSTNQKATYSFTAQSGKPLKISLVWSDAPASTTA 360

Qy 361 SVTLVNDLDLIVITAPNGTOYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLDLIVITAPNGTKVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGQPTFSLAIVN 434
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Db 300 PSQDQGRVTLTKSLAVYVNEATALTQOKATYSFQTAGKPLKLSLWTDAPGSTTA 359
Qy 361 SVTLVNDLVLITAPNGQYVGNDFSTPYNDNWDGRNNVENVFNAPOSGTYTIEVOAYN 420
Db 360 SYTLVNDLVLITAPNGQYVGNDFSTPYNDNWDGRNNVENVFNAPOSGTYTIEVOAYN 419
Qy 421 VPVGPQTFSLAIVN 434
Db 420 VPSGQRFSLAIVH 433

RESULT 7
Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROC;
OS Bacillus sp. Y.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RX MEDLINE=20568675; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046404; BAB21267.1; -; Genomic_DNA.
DR HSP; Q45670; 1-433.
DR SMR; Q9AQR2; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_S8_S53.
DR InterPro; IPR000209; Peptidase_S8; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
FT TER 433
SQ SEQUENCE 433 AA; 45588 MW; B81291A803C775AE CRC64;

Query Match 88.5%; Score 1987.5; DB 2; Length 433;
Best Local Similarity 87.3%; Pred. No. 2.7e-122;
Matches 379; Conservative 29; Mismatches 25; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQNNVGLYQGGQVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NASDPNGHGHVAGSVLNG-ALNKGMAPQANLVFQSIMDSGGGLGGLPSNLTLFSQAWN 119

Qy 121 AGARIHTNSWGAAYNGAYTTDSRVVDYVRKNVTILFAAGNEPNGGTTISAPCTAKNAI 180
Db 120 AGARIHTNSWGAAYNGAYTANSRQVDEYVRNNDMTVLFAAGNEPNSGTTISAPCTAKNAI 179

Qy 181 TVGATENLRPSFGSYADININHAOFSSRGPTKGRKIPDVMAPTFTILSARSSLPDSSF 240
Db 180 TVGATENVRPSFGSIANDPNHIAOFSSRGATRGRIKIPDVTAPTFTILSARSSLPDSSF 239

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 300
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Db 240 WANYSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGADIGLY 299
Qy 301 PNCNCGWGRVTLTKSLAVYVNEATALTQOKATYSFQTAGKPLKLSLWTDAPGSTTA 360
Db 300 PNCNCGWGRVTLTKSLAVYVNEATALTQOKATYSFQTAGKPLKLSLWTDAPGSTTA 359
Qy 361 SVTLVNDLVLITAPNGQYVGNDFSTPYNDNWDGRNNVENVFNAPOSGTYTIEVOAYN 420
Db 360 SYTLVNDLVLITAPNGQYVGNDFSTPYNDNWDGRNNVENVFNAPOSGTYTIEVOAYN 419
Qy 421 VPVGPQTFSLAIVN 434
Db 420 VPSGQRFSLAIVH 433

RESULT 8
Q4NB18_9MICC PRELIMINARY; PRT; 697 AA.
AC Q4NB18;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFNames=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitiuck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHG0100025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;

Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.1e-48;
Matches 209; Conservative 73; Mismatches 138; Indels 85; Gaps 14;

Qy 1 NDVARGIVKADVAQSSYGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITALYALGRT- 59
Db 196 NNVAEILNADVQLNGTTRVGAGEVAVADTGTDTG-DAANPHAPFTGRVQTLVALGRTA 254

Qy 60 -NNANDTNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGGLPSNLQ 112
Db 255 PDKADDPHGHTGHVAGSVLNGRNSATWGGAIEGTAPEALLILOSLDLPNGGLGGIPVNLN 314

Qy 113 TLFQAYSAGARHTNSWGA-AVNGAYTTDSRVVDYVRKN-DMTILFAAGNEGPNG--- 167
Db 315 DLFQKTYDDGARVHTNSWGVPLNLPDYASSRIDEFVNHDPQVCFAGANGDVGDNDS 374

Qy 168 -----GTISAPGTAKNAITVGATENLR-----PSFGSY-----ADNINHA 203
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Db 375 GTVDSNIGSQAANKCITVGSLSLRKEFTPTSGTYWPGDPPANPVKRDQKQANPPGMV 434
Qy 204 QFSRGPTKQRIKPDVMPAGTFTILSRSSILAP-DSSFWANHDSKYAYMGTSMTATPIVA 262
Db 435 AFSSRGPTKEGRIKPDVVPAGTFTILSRNAPMGNTFGTSTDPFLFFDSGTSMTATPIVA 494
Qy 263 GNVAQLREHFVNKRGITPKPSLLKAALIAAGADIGLGY-----PNGNCGWGRVTLDK 314
Db 495 GCAAVALRETLVKNGLNFSALVKAALVNGADVLPQQYNPSEAGESPENGSGWGRVNLAR 554
Qy 315 SLNV-----AYVNESSLSLTSQKATYSF-----TATAGKP 344
Db 555 SVVLPGQPCNAGLGGGPLEGQGDSTFDIDPEVPKVAAGRRNRGPAAPALTAAGVT 614
Qy 345 LKISLWSDAPASTTASVTLVNDLVLITAPNGTYGVGNDFTSPYNDWGDGRNVNFI 404
Db 615 LKITLWSDPPGP-----QLQNDLVLILAADGSRHGNSTTA---GFDRRNVEQVLW 666
Qy 405 NAPSQGTVTIEVQAVNVPVGPQTS 429
Db 667 TGMPPGQAVIVRAFRITQFPQPYA 691

RESULT 9
Q6MKR4 DBEBA
ID Q6MKR4 DBEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
GN OrderedLocustNames=Bd2321;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842652; CAE80143.1; -; Genomic_DNA.
DR HSP; P27693; 1AH2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Protease; Signal.
FT SIGNAL 1 8 Potential.
SQ SEQUENCE 711 AA; 74914 MW; 4930050843357E5 CRC64;

Query Match 33.6%; Score 754.5; DB 2; Length 711;
Best Local Similarity 37.9%; Pred. No. 4.8e-41;
Matches 180; Conservative 77; Mismatches 145; Indels 73; Gaps 13;

Qy 18 GLYGQGVAVADTGLDTRNDSSMHEAPRGKITAYALGRITNNA-NDTNGHGHVAGSV 76
Db 243 GYAGKGQTVSMADTGLDSG-NTGATHQDFAGGVISGYPFGLWSKWSMDPMGHTHVAGSV 301
Qy 77 LONGSTNKGK-----APQANLVFQSMDSGGGLGLPLSNLQTLFSAQYAGARIHTNSWGA 132
Db 302 MGRGTASKGLLKGGAYEAMVAEGMWSMMKNLSVPSKGLDLFEKAFADGARIHTNSWG 361
Qy 133 A-VNGAYTTDSNRVDYVRKN-DMTILFAAGNEP-----NGGTISAPGTAKNAITV 182
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Db 362 ARTFGAYDNPVQVDEWSYANPDMILFAAGSGADKNKDKGRIDSNMSASPGTAKNVLTV 421
Qy 183 GATENL-----RPSFGSY-ADNINHVAQSSSRGPTKGRIKPD 219
Db 422 GASENVTKSGGIQVPIISKLAADKDEWPESEIYSSYISDNGNGLAMFSSRGPTTDGRTPKD 481
Qy 220 VMARGTPILSARSLAPDSSFWANHDSKYAYMGTSMTATPIVAGNVAQLREHFVNKRGIT- 278
Db 482 IVAPGTNVLSVVFQOEKQDASPLMGAYNKDYVWSGTSMTATPLAAGAAIAIAKQVLVEKLG 541
Qy 279 TPXPSLILKAALIAAGADIGLGY-----PNGNCGWGRVTLDKSLNVA--- 319
Db 542 NPSAALMKATMLTAVDMYFGQFGEIGAARGQELTERPNSDGYGRVDVANIANLCGAT 601
Qy 320 -YNESSLSLTSQKATYSFTATAGPKIKISLWSDAPASTTASVTLVNDLVLITAPNGT 378
Db 602 QFVDNRQGAQGAEVSYEFTINAPGSLYANLVMTDAPGSANAAQALVNDLVLITPENGQ 661
Qy 379 QYVGNDFTPSYNDWGDGRNVNFIAPQSGTVTIEVQAVNVPV---GPQTSRL 430
Db 662 TLSMNDHI-----NNLEMIKSLPAGTYKLTIVKGFQVQGNKGAQAYAL 706

RESULT 10
Q4NVB5_9DELTA
ID Q4NVB5_9DELTA PRELIMINARY; PRT; 1748 AA.
AC Q4NVB5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin:Nepovirus coat
DE protein, N-terminal:Nepovirus coat protein, N-terminal precursor.
GN ORFNames=AdenDRAFT_3007;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD0100011; EAL79523.1; -; Genomic_DNA.
KW Capsid protein; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 1748 AA; 177411 MW; BL86DE33BB81DE76 CRC64;

Query Match 32.9%; Score 739.5; DB 2; Length 1748;
Best Local Similarity 40.1%; Pred. No. 1.5e-39;
Matches 192; Conservative 66; Mismatches 154; Indels 67; Gaps 19;

Qy 1 NDVARGIVK-----ADVAQSSYGLVQGVAVADTGLD-----TGRNDSMHEAFR 47
Db 248 NDTGRWITQTVGSDTSISDRGLDQGVAVIGTGLDHDACWFRDPIGAAGPMHR---- 304
Qy 48 GKITALYALGRITNANDTN-CHGTHVAGSVLGN-----GSTNKGMAPQANLVFQSI 100
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Df 305 -KVAAYITVG--GDDYDGNLGHGTHVAGTQDPTITGAAANMGAPGVVVVDLFLG 361
Qy 101 GGGGLGGLPSNLQTLFQAYSAGARIHTNSWGAANVAGYTTDSRNVDYVRKN-DMTILFA 159
Df 362 ENWFSPADLAETFTFYALGARIHTNSWSSN-AYDALARSADRFMEHPDFVLFA 420
Qy 160 AGNEGPNGGTISAGTAKNAITVGATENLRFSGSYADNINHNHVAQFSSRGPTKGRKPD 219
Df 421 NGNAGPDVGSVGPATARNVSVGATGN-----GLAAED--VASFSSHGPAADGRTKPT 472
Qy 220 VMAPGTTILSARSLAPDSSFWANHDSKYAVMGCTSMATPIVAGNVAQLREHFVN---R 276
Df 473 LTAPEGVGLVSADSGTTPAS-----NCSSTVAF-SGTSMATPAAAGAAALVRQYFEGGFWS 527
Qy 277 GI-----TPKPSLLKAAIAGAADI-----GLG-YPNGNGMGRTVLDKSLNVA----- 319
Df 528 GLGSPADARSFSAALVKATLVNSAQVAGENGPISTGGWGRINLSNALRFAADAAY 587
Qy 320 --YNESSSLTSOKATYSFTATAGKPLKISLWSDAPASTTASVTLVNDLVLVITAPNG 377
Df 588 LDVVEVAAGLETGGSFTRQVFSTGAQPLKLTVLWTDAPGSQLADRSVLNVDLVLAVTPGG 647
Qy 378 -TQVVGNDFT---SPYNDNDGRNVNFINAPQSGTYTIEVQAYNVVPGQPTFSLAI 432
Df 648 ATTILGNVFLGESVAGGAPRLNVEBQVLLAAPTGYTIVRTGYNVVPGQPPFALVI 706

RESULT 11
Q4HUY5 GIBZE
ID Q4HUY5_GIBZE PRELIMINARY; PRT; 1088 AA.
AC Q4HUY5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=FGL1223.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ranasingh U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuppback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AACW01000460; EAA75433.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1088 AA; 119629 MW; E3B38CB94C07F542 CRC64;
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Query Match 26.3%; Score 592; DB 2; Length 1088;
Best Local Similarity 35.6%; Pred. No. 4e-30;
Matches 181; Conservative 71; Mismatches 170; Indels 86; Gaps 24;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVADPTGLDGTGRNDSSM-----HEAPRGKITAYAL 56
Df 581 NDLAETLTANILALSTSYEGNGQKVCVADTGTDOGMADMGILVHPAFNGRVEHLEAL 640
Qy 57 GRTNNANDTNGHGTTHVAGSVLNGSTN-----KGMAPQANLVFOSI-----MDSGGGLGG 106
Df 641 W-LGDSKDTAGHGTWCASICGNGLYKNGDIRVGVAPGATLMVQSLAQVSRDPNKGAI 699
Qy 107 LPSNL-QTLFQAYSAGARIHTNSWGA---AVNG--AYTTDSRNVDYV-RKNDMTILFA 159
Df 700 VPMDLGLQLFSNPYKLYRHSNSGWKWDKATGQLGYEQAWDIDKFVIDHQDFVVLVA 759
Qy 160 AGNEGPNGGT-----ISAPGTAKNAITVGATENLRPSFGSYADN-----INHVAQFS 206
Df 760 AGNNAEKAKSKSNHIGAAGSAFNCITVGATGTTTPNNNDYGFNEVGAKPMTRINDTAKFS 819
Qy 207 SRGPTKD-----GRIKPDVMAPTFILSARS-SLAPDS-----SFWANHDSKYAYM 251
Df 820 SRGPTKPRDINGNEVAGRIKPDVAPGVALLSAAARAWAKOSRNRVMYGRGTGDDMTFM 879
Qy 252 GGTSMATPIVAGNVAQLREHFVNRIKPKPSLLKAAIAGAAD-----IGLGYPNNGN 305
Df 880 SGTSMTPLVAGCVALLREALKHEKGPAAALIKALLVNGAVNFSQGLGLGY-DYDQ 938
Qy 306 GMRVTLTKSLNV-----AYNESSSLTSQ-----KATYS-FTATAGK-PL 345
Df 939 GGRVDIDSSISIMVLSVDFGDKLPEDTQFDVAPLRQVPEEERRWTSSLIPVAGNRNL 998
Qy 346 KISLWSDAPASTTASVTLVNDLVLVITAPNGYQYVNDFTSPYNDWMDGRNVDNFIN 405
Df 999 TVTLAYPDPAQ---SGLMNDINLIVLS-GGAERHGMKGKGP---GYDHTNNVEKLIWE 1051
Qy 406 APOSGTYTIEVQAY-NVPV-GPOTFSLA 431
Df 1052 NVPGTFKIVASIMNIDVKAPTSFAVA 1079

RESULT 12
Q747P6 GEOSL
ID Q747P6 GEOSL PRELIMINARY; PRT; 2030 AA.
AC Q747P6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fibronectin type III domain protein.
GN OrderedLocusNames=GSU3219;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Maduprat R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gunn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouir H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.B., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR ENBL; AS017180; AAR36610.1; -; Genomic_DNA.
DR HSP; P27693; IAH2.
DR TIGR; GSU3219; -.
DR GO; GO:0004289; F:subtilase activity; IEA.
```



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Db 725 MSNHLVNNNNNNNNKTSIGITKFGVIGGLDLRLVKPNQWKEESLSTGNTSYCTYK 784
Qy 339 -----ATAGPKLK--ISLVMSDAPASTTASVTLVNDLVI-----TAPNGT 378
Db 785 PSSSSSSGNNIPRVVATLVWTDPPSVAGAKFNLVNNLDLMTIYYRONGSTIFYSNQGS 844
Qy 379 QYVGNDFTSPYNDWMDGRNNVNFVINAPOSQGTITIEVQAYNVVPGQTF 429
Db 845 SFLG--LAPQDT--LNNVEGIVHNPTEPMTYREWVAGTNVPMGPQNS 889

RESULT 14
TAGC DICDI
ID TAGC DICDI STANDARD; PRT; 1743 AA.
AC Q23868;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prestalk-specific protein tagc precursor (BC 3.4.21.-).
GN Name=tagc;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=AX4;
RX MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
RA Shauleky G., Escalante R., Loomis W.F.;
RT "Developmental signal transduction pathways uncovered by genetic suppressors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
CC -!- FUNCTION: Intercellular communication via tagc may mediate integration of cellular differentiation with morphogenesis (By similarity).
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -!- SIMILARITY: Contains 1 peptidase S8 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL: U60086; AAB03331.1; -; mRNA.
DR PIR: T18279; T18279.
DR HSP: P08716; IMT0.
DR DictyBase; DB0001795; tagc.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC TM transpt.
DR InterPro; IPR003439; ABC_transp.like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00664; ABC membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000006; ABC transporter; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
KW ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease; Serine protease; Signal; transmembrane; transport.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1743 Prestalk-specific protein tagc.
FT TRANSMEM 962 982 Potential.
FT TRANSMEM 1027 1047 Potential.
FT TRANSMEM 1072 1092 Potential.
FT TRANSMEM 1157 1177 Potential.
FT TRANSMEM 1260 1280 Potential.
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FT TRANSMEM 1288 1308 Potential.
FT DOMAIN 1031 1314 ABC transmembrane type-1.
FT DOMAIN 1450 1687 ABC transporter.
FT NP_BIND 1485 1492 ATP (Potential).
FT REGION 316 642 Serine protease.
FT COMPBIAS 42 46 Poly-Asn.
FT COMPBIAS 94 103 Poly-Asn.
FT COMPBIAS 643 646 Poly-Ala.
FT COMPBIAS 733 741 Poly-Asn.
FT COMPBIAS 786 792 Poly-Ser.
FT COMPBIAS 1337 1340 Poly-Glu.
FT COMPBIAS 1346 1352 Poly-Gly.
FT COMPBIAS 1353 1357 Poly-Asn.
FT COMPBIAS 1358 1364 Poly-Asp.
FT COMPBIAS 1381 1386 Poly-Asn.
FT COMPBIAS 1707 1729 Poly-Asn.
FT ACT_SITE 325 325 Charge relay system (By similarity).
FT ACT_SITE 372 372 Charge relay system (By similarity).
FT ACT_SITE 637 637 Charge relay system (By similarity).
FT CARBOHYD 390 390 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 614 614 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 689 689 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 741 741 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 776 776 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 832 832 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 887 887 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 1251 1251 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 1385 1385 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 1386 1386 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 1454 1454 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 1704 1704 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 1743 AA; 12DB363E2F729839 CRC64;

Query Match 23.3%; Score 523.5; DB 1; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

Qy 19 LYQGOIVAVADTGLTGR---NDS-----SMHEAFRGKITALYALGFTNNANDTNGH 68
Db 314 LRKGQILSIADTGLDGHCHCFSDSKYPIPLNSVLNHR-KVVTYITTSDDSDKVDGH 372
Qy 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLTFLSQAY 119
Db 373 GTHICGSAAGTPEDSSVNISSFGLATDAXIAE--FDLASGSSSLTFPSDLKQLQPLY 429
Qy 120 SAGARIHTNSWGA----AVNGAYTTDSRNVDYVRKN-DWTILFAAGNPGNGGTIS--A 172
Db 430 DAGARVHCDSWGVSVEGVTGYSSTASIDDFLTHPDIILRAAGN---NEQYLSLLT 486
Qy 173 PGTAKNAITVGATENLR-----PSGSYADNI----- 199
Db 487 QSTAKNVIITGAHQTHENYLTDPNINYNQSVNDINQELICDFDSRYCNYTTAQCCLES 546
Qy 200 -----NHVAOFSSRGPTKDGRIKPDVMAPGTFIL 228
Db 547 NATTGASCCPTLLRKSVDAIDAANTQPLLNNENNICSFSKGPETHDGMKALVAPGYIT 606
Qy 229 SARSSIA-----PDSSFNANHDSKYVMGTSMTATPIVAGNVAQLREH-----F 272
Db 607 SARSGNANTDQCGDGLS-PNTNALLA-ISGTSMTATSFAAAAATILRQYLVVDGYPTGSI 664
Qy 273 VKNRGITPSPSLKALIAIGA-----ADIGLYPNGN-----QGWGRVT 311
Db 665 VESNKLOPTGSLKALMINNAQLNGTFOLITSSSITYPSNQVFENFAGASLVQGGAIR 724
Qy 312 LDKSLNVAVYNESS-----SLTSQKATYSFT-- 338
Db 725 MSNHLVNNNNNNNNKTSIGITKFGVIGGLDLRLVKPNQWKEESLSTGNTSYCTYK 784
Qy 339 -----ATAGPKLK--ISLVMSDAPASTTASVTLVNDLVI-----TAPNGT 378
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Db	785	PSSSSSNGNIPRVVATLVWTDPPSYAGAKFNVLNLDLTMIIYRDRNGSTIYFSNQGS	844
Qy	379	QYVGNDFTSPYNDNDGRNVVENFVINAPOSGTYTIEQYQVNVVPGQFES	429
Db	845	SFLG---LAPTQDT--LNNVEGIVHNPTETPVFVNVAGTIVDMPGQFES	889
RESULT 15			
Q8T9W1	DICD1		
ID	Q8T9W1	DICD1 PRELIMINARY;	PRT; 1825 AA.
AC	Q8T9W1;		
DT	01-JUN-2002	(T-EMBLrel. 21, Created)	
DT	01-JUN-2002	(T-EMBLrel. 21, Last sequence update)	
DT	10-MAY-2005	(T-EMBLrel. 30, Last annotation update)	
DE	Serine protease/ABC transporter TagD (ABC transporter B family protein).		
GN	Name=tagd; ORFNames=DOB0191427;		
OS	Dictyostellum discoideum (Slime mold).		
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.		
OX	NCBI_TaxID=44689;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Ax4;		
RC	STRAIN=Ax4;		
AN	Anjard C., Loomis W.F.;		
RL	Submitted (JAN-2002)	to the EMBL/GenBank/DBJ databases.	
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Ax4;		
RA	Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,		
RA	Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,		
RA	Tungkal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,		
RA	Bankal A.T., Lemmehann R., Hamlin N., Davies R., Gaudet P., Fey P.,		
RA	Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,		
RA	Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,		
RA	Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,		
RA	Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,		
RA	Muzny D., Mourlet T., Pain A., Lu M., Harper D., Lindsay R.,		
RA	Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,		
RA	Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,		
RA	Louleged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,		
RA	Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Tivey A.,		
RA	Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,		
RA	Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,		
RA	Shaulesky G., Schleichner M., Weinstein G., Rosenthal A., Cox E.C.,		
RA	Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,		
RA	Williams J., Dear P.H., Noegel A.A., Barrell B., Kasper A.;		
RT	"the genome of the social amoeba Dictyostellum discoideum.";		
RL	Nature 010-00057.		
RL	EMBL; AF46309; AAL74253.1; -; Genomic_DNA.		
DR	EMBL; AF01000133; EAL64354.1; -; Genomic_DNA.		
DR	HSP; P08716; LMT0.		
DR	DictyBase; DOB0191427; tagD.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0016887; F:ATPase activity; IEA.		
DR	GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.		
DR	GO; GO:0000166; F:nucleotide binding; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004289; F:subtilase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	GO; GO:0006810; P:transport; IEA.		
DR	InterPro; IPR003593; AAA_AFPase.		
DR	InterPro; IPR011527; ABC membrane_1.		
DR	InterPro; IPR001140; ABC_TM_transp.		
DR	InterPro; IPR003439; ABC_transp_like.		
DR	InterPro; IPR000209; Pept_S8_S53.		
DR	Pfam; PF00664; ABC membrane_1.		
DR	Pfam; PF00005; ABC_tran; 1.		
DR	Pfam; PF00082; Peptidase_S8; 1.		
DR	PRINTS; P00723; SUBTILISIN.		
DR	PRODOM; PD000006; ABC transporter; 1.		
DR	SMART; SM00382; AAA; 1.		

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 08:25:46 ; Search time 189 Seconds
(without alignments)
1008.944 Million cell updates/sec

Title: US-10-820-712A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAVNPVGPQTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

A_Geneseq_21.*
1: Genesexp1990s.*
2: Genesexp1990s.*
3: Genesexp2000s.*
4: Genesexp2001s.*
5: Genesexp2002s.*
6: Genesexp2003as.*
7: Genesexp2003bs.*
8: Genesexp2004s.*
9: Genesexp2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2247	100.0	434	5	AAM50080
2	2247	100.0	434	7	ADY33778
3	2247	100.0	434	7	ADZ51757
4	2247	100.0	434	8	ADL25802
5	2247	100.0	434	8	ADTM40771
6	2247	100.0	434	8	ADSI4442
7	2247	100.0	434	8	ADT49604
8	2247	100.0	640	2	AAV17090
9	2247	100.0	640	8	ADM40773
10	2247	100.0	640	8	ADSI4437
11	2247	100.0	641	8	ADTM40771
12	2242	99.8	434	8	ADTM40780
13	2242	99.8	434	8	ADSI4441
14	2242	99.8	640	2	AAV17091
15	2239	99.6	434	8	ADSI4438
16	2239	99.6	434	8	ADSI4442
17	2238	99.6	434	8	ADSI4439
18	2232	99.3	434	8	ADSI4440
19	2230	99.2	434	8	ADSI4443
20	2225	99.0	434	8	ADSI4444
21	2210	98.4	434	8	ADSI4445
22	2195	97.7	436	8	ADM40787
23	2191	97.5	434	5	AAM50081
24	2191	97.5	434	7	ADZ51758

CC	additives, food modifiers and pharmaceutical compositions. The alkaline protease may also be used as bleaching detergent, hard surface cleansing detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing cleanser for medical tools. The new alkaline protease has a more potent proteolytic capacity, exhibiting excellent detergency for the removal of a complex stain, and has high secretion capacity. This sequence corresponds to the <i>Bacillus sp.</i> alkaline protease.
XX	
SQ	Sequence 434 AA;
	Query Match 100.0%; Score 2247; DB 7; Length 434;
	Best Local Similarity 100.0%; Pred. No. 6.4e-159;
	Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 NDVARGIVKADVAQSSYGLYGQGQI VAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
DB	1 NDVARGIVKADVAQSSYGLYGQGQI VAVADTGLDTGRNDSMHEAFRGKITALVALGRTN 60
QY	61 NANDTNHGHTHVAGSVLGNSTNGMAPOANLVFQSIMDGGGLGGLPSNLQTILFSQAYS 120
DB	61 NANDTNHGHTHVAGSVLGNSTNGMAPOANLVFQSIMDGGGLGGLPSNLQTILFSQAYS 120
QY	121 AGARIHNTNSWGAAVNGAYTTDSRNVDYVRKNDMTILPAAGNEGPGGTISAPGTAKNAI 180
DB	121 AGARIHNTNSWGAAVNGAYTTDSRNVDYVRKNDMTILPAAGNEGPGGTISAPGTAKNAI 180
QY	181 TVGATENLRSPFGSYADINIHVAFSSRGP TKGR IKPDVMAPCTFILSARSSLAPDSSF 240
DB	181 TVGATENLRSPFGSYADINIHVAFSSRGP TKGR IKPDVMAPCTFILSARSSLAPDSSF 240
QY	241 WANHDSKIAYMGGTSMATPIVAGNVAQOLREHFVKNRGITPKPSLLKAALIAGAADI GLGY 300
DB	241 WANHDSKIAYMGGTSMATPIVAGNVAQOLREHFVKNRGITPKPSLLKAALIAGAADI GLGY 300
QY	301 PNGNQGWGRVTLDKSLNVA YVNES SSI STSQATYSFTATAGKPLK I SLVMSDAPASTTA 360
DB	301 PNGNQGWGRVTLDKSLNVA YVNES SSI STSQATYSFTATAGKPLK I SLVMSDAPASTTA 360
QY	361 SVTLVNDL DLVI TAPNGTQYVGNDFTSPYNDNWGRNNVENVF INAPQSGTYTIEVOAYN 420
DB	361 SVTLVNDL DLVI TAPNGTQYVGNDFTSPYNDNWGRNNVENVF INAPQSGTYTIEVOAYN 420
QY	421 VPVGPQTFLSAIVN 434
DB	421 VPVGPQTFLSAIVN 434
RESULT 3	
ADZ51757	ID ID ADZ51757 standard; protein; 434 AA.
XX	AC ADZ51757;
XX	XX XX 16-JUN-2005 (first entry)
XX	DE DE Wild-type Bacillus sp. alkali protease.
XX	XX alkali protease; enzyme; surfactant; mutagenesis.
XX	XX Bacillus sp.
OS	OS JP2003125783-A.
PX	PX 07-MAY-2003.
XX	XX 26-OCT-2001; 2001JP-00329472.
PF	PF 26-OCT-2001; 2001JP-00329472.
PR	PR (KAOS) KAO CORP.
XX	XX WPI; 2003-856569/80.
DR	XX
XX	XX

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XX alkaline protease; washing agent; enzyme.
KW Bacillus sp.
XX JP2004008085-A.
XX 15-JAN-2004.
XX 06-JUN-2002; 2002JP-00165950.
XX 06-JUN-2002; 2002JP-00165950.
XX (KAOS ) KAO CORP.
XX WPI; 2004-094297/10.
XX N-PSDB; ADL25803.
XX Novel mutant alkaline protease produced by substituting the amino acid
PT residues useful as washing agent.
XX Claim 1; SEQ ID NO 1; 21pp; Japanese.
XX The invention comprises a mutant Bacillus alkaline protease which
CC contains substitutions at positions 163, 170 and 434. The mutant alkaline
CC protease is useful as a washing agent. The present amino acid sequence
CC represents a Bacillus alkaline protease of the invention.
XX Sequence 434 AA;
SQ
Query Match 100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNHGHTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNHGHTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARLHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARLHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
DB 181 TVGATENLRPFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLDLVITAPNGTQYVGNDETSPYNDKWDGNNVNFVINAPOSQGTVTIEVOAYN 420
DB 361 SVTLVNDLDLVITAPNGTQYVGNDETSPYNDKWDGNNVNFVINAPOSQGTVTIEVOAYN 420
QY 421 VPGVQTFSLAIYN 434
DB 421 VPGVQTFSLAIYN 434
RESULT 5
ADM40771
ID ADM40771 standard; protein; 434 AA.
XX
AC ADM40771;
XX

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DT 01-JUL-2004 (first entry)
XX Mature alkaline protease from Bacillus sp. KSM-KP43.
XX alkaline protease; laundry detergent; bleaching agent; detergent;
XX denture-cleaning agent; enzyme.
XX Bacillus sp.; KSM-KP43.
XX US2004072321-A1.
XX 15-APR-2004.
XX 09-JUN-2003; 2003US-00456479.
XX 26-JUN-2002; 2002JP-00186387.
XX 18-OCT-2002; 2002JP-00304232.
XX (KAOS ) KAO CORP.
XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
XX WPI; 2004-328572/30.
XX N-PSDB; ADM40772.
XX New alkaline protease having a mutant prepro sequence where amino acid
PT residues at positions 52, 75 and 142 are substituted with another amino
PT acid residue, useful as enzyme component of laundry detergents, or
PT bleaching agents.
XX Claim 1; SEQ ID NO 2; 29pp; English.
XX The invention relates to an alkaline protease having a prepro sequence.
CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
CC acid residues at: (a) position 52 is substituted by aspartic acid or
CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
CC position 142 is substituted by lysine. The alkaline protease is useful as
CC an enzyme which can be incorporated into laundry detergents, bleaching
CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
CC cleaning agents, and detergents for sterilising medical apparatus. The
CC present sequence represents mature alkaline protease from Bacillus sp.
XX KSM-KP43.
XX Sequence 434 AA;
SQ
Query Match 100.0%; Score 2247; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNHGHTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNHGHTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARLHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARLHTNSWGAANVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
DB 181 TVGATENLRPFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSSSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

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Qy	361	SVTLVNDLVLVITAPNGTQYVGNDFTSPYNDNWGRNNVENVFINAPQSGTTYTIEVOAYN	420
Dd	361	SVTLVNDLVLVITAPNGTQYVGNDFTSPYNDNWGRNNVENVFINAPQSGTTYTIEVOAYN	420
Qy	421	VPVGPOTFSLAIWN	434
Dd	421	VPVGPOTFSLAIWN	434
 RESULT 6 ADSI4427			
ID	ADS14427 standard; protein; 434 AA.		
XX	AC		
XX	ADSI4427;		
DT	30-DEC-2004 (first entry)		
XX			
DE	Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.		
XX			
KW	protease; enzyme; alkaline protease; laundry detergent; KP43.		
OS	Bacillus sp.; KSM-KP43.		
XX			
PN	<u>EPI456962-A1.</u>		
XX	13-OCT-2004.		
XX			
Pf	08-APR-2004; 2004EP-00008604.		
XX			
PR	10-APR-2003; 2003JP-00106709.		
XX	(KAOS) KAO CORP.		
PA			
XX			
PI	Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayaashi T;		
XX			
DR	WPI; 2004-711313/70.		
N-PSDB;	ADSI4428.		
XX			
PT	New engineered alkaline protease, useful particularly in laundry		
PT	detergents, comprising specified amino acids at particular positions.		
XX			
PS	Claim 1; SEQ ID NO 1; 31pp; English.		
XX			
CC	The invention relates to a novel alkaline protease. The new alkaline		
CC	protease comprises an amino acid sequence in which one or more amino acid		
CC	residues selected from those located at 7 specific positions within		
CC	ADSI4427, or at positions corresponding to these positions are: position		
CC	15 (histidine), position 16 (threonine or glutamine), position 166		
CC	(glycine), position 167 (valine), position 187 (serine), position 346		
CC	(arginine), and position 405 (aspartic acid). The alkaline protease is		
CC	useful in industry particularly in laundry detergents, but also e.g. in		
CC	fibre modifying agents, leather processing agents, cosmetic compositions,		
CC	bath additives, food-modifying agents, and pharmaceuticals. The present		
CC	sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline		
CC	protease, KP43.		
XX			
SQ	Sequence 434 AA;		
 Query Match 100.0%; Score 2247; DB 8; Length 434; Best Local Similarity 100.0%; Pred. No. 6.4e-159; Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
Qy	1	NDVARGIVKADVAAQSISGLYGOGQIVAVADTGLDTRGNDSSMHEAFRGKITALYALGRTN	60
Dd	1	NDVARGIVKADVAAQSISGLYGOGQIVAVADTGLDTRGNDSSMHEAFRGKITALYALGRTN	60
Qy	61	NANDTNGHGTTHVAGSVLGNSTNKGMWFOANLWFQSIMDSGGGLGGLPSNLQTLFSOAYS	120
Dd	61	NANDTNGHGTTHVAGSVLGNSTNKGMWFOANLWFQSIMDSGGGLGGLPSNLQTLFSOAYS	120
Qy	121	AGARIHTNSGWAANGAYTTDSRNVDYVRKNDMTILFAAGNEPGNGTISAFPCTAKNAI	180

QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAFRGKITALYALGRTN 60
 DB 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAFRGKITALYALGRTN 60
 QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
 DB 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
 QY 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 DB 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
 DB 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
 QY 301 PNGQGWGRVTLDKSLNVAAYNNESSLSSTSQATYSFTATAGKPKISLVMSDAPASTTA 360
 DB 301 PNGQGWGRVTLDKSLNVAAYNNESSLSSTSQATYSFTATAGKPKISLVMSDAPASTTA 360
 QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNDVNFNAPQSGTYYTIEVQAYN 420
 DB 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNDVNFNAPQSGTYYTIEVQAYN 420
 QY 421 VPVGPQTFSLAIVN 434
 DB 421 VPVGPQTFSLAIVN 434

RESULT 8
 AAY17090
 ID AAY17090 standard; protein; 640 AA.
 AC AAY17090;
 XX
 XX
 DT 20-MAR-2003 (revised)
 DT 21-JUL-1999 (first entry)
 XX
 DE Bacillus alkaline protease.
 XX
 XX Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
 KW washing composition; oxidising agent.
 XX
 OS Bacillus sp.
 XX
 PN WO9918218-Al.
 XX
 PD 15-APR-1999.
 XX
 PF 07-OCT-1998; 98WO-JP004528.
 XX
 PR 07-OCT-1997; 97JP-00274570.
 XX
 XX (KAOS) KAO CORP.
 XX
 PI Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
 PI Shikata S, Nomura M;
 XX
 XX WPI; 1999-287736/27.
 DR N-PSDB; AAX3278.
 XX
 XX Alkali protease from Bacillus used in washing powders.
 PT
 PS Disclosure; Page 58-63; 71pp; Japanese.
 XX
 XX The invention relates to alkaline proteases produced by strains of
 CC Bacillus. The proteases alkali to digest casein is not inhibited by
 CC oleic acid and they have a high stability to oxidising agents. The
 CC alkaline protease of the invention has the following properties: (a) it

CC is active over the pH range 4-13 and has at least 80% of its optimum
 CC activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is
 CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
 CC its ability to digest casein is not inhibited by oleic acid; (e) it has
 CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
 CC used as enzymes in washing compositions for use in automatic dishwashers
 CC and for washing clothes. The stability to oxidising agents allows the
 CC enzyme to be an effective component of washing compositions including
 CC bleaches. The present sequence represents an alkaline protease. (Updated
 CC on 20-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 2; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.le-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAFRGKITALYALGRTN 60
 DB 207 NDVARGIVKADVAQSSVGLYGQGIIVAVADTGLTGRNDSSMHEAFRGKITALYALGRTN 266
 QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 120
 DB 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFQAYS 326
 QY 121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 DB 327 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
 QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 240
 DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTILSARSSLPDSSF 446
 QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
 DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 506
 QY 301 PNGQGWGRVTLDKSLNVAAYNNESSLSSTSQATYSFTATAGKPKISLVMSDAPASTTA 360
 DB 507 PNGQGWGRVTLDKSLNVAAYNNESSLSSTSQATYSFTATAGKPKISLVMSDAPASTTA 566
 QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNDVNFNAPQSGTYYTIEVQAYN 420
 DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRNNDVNFNAPQSGTYYTIEVQAYN 626
 QY 421 VPVGPQTFSLAIVN 434
 DB 627 VPVGPQTFSLAIVN 640

RESULT 9
 ADM40773
 ID ADM40773 standard; protein; 640 AA.
 AC ADM40773;
 XX
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Alkaline protease from Bacillus sp. KSM-KP43.
 XX
 KW alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX
 OS Bacillus sp.; KSM-KP43.
 XX
 PN US2004072321-A1.
 XX
 PD 15-APR-2004.
 XX
 PF 09-JUN-2003; 2003US-00456479.
 XX
 PR 26-JUN-2002; 2002JP-00186387.
 PR 18-OCT-2002; 2002JP-00304232.

XX (KAOS) KAO CORP.
XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
XX WPI; 2004-328572/30.
XX N-PSDB; ADM40772.
XX New alkaline protease having a mutant prepro sequence where amino acid
XX residues at positions 52, 75 and 142 are substituted with another amino
XX acid residue, useful as enzyme component of laundry detergents, or
XX bleaching agents.
XX Disclosure; SEQ ID NO 4; 29pp; English.
XX
XX The invention relates to an alkaline protease having a prepro sequence.
XX The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
XX acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
XX acid residues at: (a) position 52 is substituted by aspartic acid or
XX arginine; (b) position 75 is substituted by alanine or arginine; and (c)
XX position 142 is substituted by lysine. The alkaline protease is useful as
XX an enzyme which can be incorporated into laundry detergents, bleaching
XX agents, detergents for cleaning hard surfaces or drainpipes, denture-
XX cleaning agents, and detergents for sterilising medical apparatus. The
XX present sequence represents alkaline protease from *Bacillus* sp. KSM-KP43.
XX
XX Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.le-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDPVMAQPTFTLSARSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDPVMAQPTFTLSARSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
QY 301 PNGNOGGRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNOGGRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVNFVINAPOSQGTYYIEVOAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVNFVINAPOSQGTYYIEVOAYN 626
QY 421 VPVGPQTFFSLAIVN 434
DB 627 VPVGPQTFFSLAIVN 640

RESULT 10
ADSL4437
ID ADS14437 standard; protein; 640 AA.
XX AC
XX ADS14437;
XX
XX 30-DEC-2004 (first entry)
XX DT
XX

DE *Bacillus* alkaline protease KP43.
XX
XX protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
XX *Bacillus* sp.; KSM-KP43.
XX
XX Key Location/Qualifiers
XX Peptide 1..206
XX Protein 207..640
XX
XX EPI466962-A1.
XX
XX 13-OCT-2004.
XX
XX 08-APR-2004; 2004EP-00008604.
XX
XX 10-APR-2003; 2003JP-00106709.
XX
XX (KAOS) KAO CORP.
XX
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX WPI; 2004-711313/70.
XX N-PSDB; ADS14428.
XX
XX New engineered alkaline protease, useful particularly in laundry
XX detergents, comprising specified amino acids at particular positions.
XX
XX Disclosure; SEQ ID NO 1; 31pp; English.
XX
XX The invention relates to a novel alkaline protease. The new alkaline
XX protease comprises an amino acid sequence in which one or more amino acid
XX residues selected from those located at 7 specific positions within
XX ADS14427, or at positions corresponding to these positions are: position
XX 15 (histidine), position 16 (threonine or glutamine), position 166
XX (glycine), position 167 (valine), position 187 (serine), position 346
XX (arginine), and position 405 (aspartic acid). The alkaline protease is
XX useful in industry particularly in laundry detergents, but also e.g. in
XX fibre modifying agents, leather processing agents, cosmetic compositions,
XX bath additives, food-modifying agents, and pharmaceuticals. The present
XX sequence represents the wild-type *Bacillus* sp. KSM-KP43 alkaline
XX protease, KP43. The sequence is shown in the sequence listing as part of
XX SEQ ID NO:1
XX
XX Sequence 640 AA;
Query Match 100.0%; Score 2247; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.le-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDPVMAQPTFTLSARSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKDPVMAQPTFTLSARSLAPDSSF 446
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
QY 301 PNGNOGGRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNOGGRVTLDKSLNVAYNVNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
 Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
 Db 627 VPVGPQTFSLAIVN 640

RESULT 11
 ADT49613
 ID ADT49613 standard; protein; 641 AA.
 XX AC ADT49613;
 XX DT 30-DEC-2004 (first entry)
 XX DE Bacillus alkaline protease.
 XX KW Alkaline protease; detergent; fiber modification; leather processing;
 KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
 XX OS Bacillus sp. KSM-KP43.
 XX FH Key Location/Qualifiers
 FT Peptide 1..206
 FT Protein /note= "signal peptide"
 FT Protein 207..641
 FT Protein /note= "specifically claimed mature protein (SEQ ID 1)"
 XX EPI466970-Al.
 PN 13-OCT-2004.
 PD 08-APR-2004; 2004EP-00008605.
 XX 10-APR-2003; 2003JP-00106708.
 XX (KAOS) KAO CORP.
 PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
 XX WPI; 2004-711317/70.
 DR N-PSDB; ADT49605.
 XX New engineered alkaline protease with improved activity and thermal
 PT stability, useful particularly in detergents such as laundry detergents.
 XX Disclosure; Page 19-25; 35pp; English.
 XX The invention relates to an alkaline protease and its encoding gene. The
 CC alkaline protease can be expressed by standard recombinant methodology.
 CC The alkaline protease is useful in the industry particularly in
 CC detergents such as laundry detergents, but also in fiber modifying
 CC agents, leather processing agents, cosmetic compositions, bath additives,
 CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
 CC and thermal stability. The present sequence represents an alkaline
 CC protease from Bacillus sp. KSM-KP43.
 XX SQ Sequence 641 AA;
 Query Match 100.0%; Score 2247; DB 8; Length 641;
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 60
 Db 207 NDVARGIVKADVAQSSYGLYGQGIQVAVADTGLDTRNDSSMHEAFRGKITALVALGRTN 266

Qy 61 NANDTNGHGTAVAGSVLGNSTKGMAPQANLVFQISMDSGGGLGGLPSNLQTLFSQAYS 120
 Db 267 NANDTNGHGTAVAGSVLGNSTKGMAPQANLVFQISMDSGGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSWGAUNGAAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
 Db 327 AGARIHTNSWGAUNGAAYTTDSRVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIKPDVMAFGTFLSARSSILAPDSSF 240
 Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKGRIKPDVMAFGTFLSARSSILAPDSSF 446

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLY 300
 Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAAIAGAADIGLY 506

Qy 301 PNGQGWGRVTLDKSLNVAYVNESSLSLTSQKATYSATATAGPKLSLVMSDAPASTTA 360
 Db 507 PNGQGWGRVTLDKSLNVAYVNESSLSLTSQKATYSATATAGPKLSLVMSDAPASTTA 566

Qy 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
 Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626

Qy 421 VPVGPQTFSLAIVN 434
 Db 627 VPVGPQTFSLAIVN 640

RESULT 12
 ADM40780
 ID ADM40780 standard; protein; 434 AA.
 XX AC ADM40780;
 XX DT 01-JUL-2004 (first entry)
 XX DE Alkaline protease #2 from Bacillus sp. KSM-KP9865.
 XX KW alkaline protease; laundry detergent; bleaching agent; detergent;
 KW denture-cleaning agent; enzyme.
 XX OS Bacillus sp.; KSM-KP9865.
 XX PN US2004072321-A1.
 XX PD 15-APR-2004.
 XX 09-JUN-2003; 2003US-00456479.
 XX 26-JUN-2002; 2002JP-00186387.
 XX 18-OCT-2002; 2002JP-00304232.
 XX (KAOS) KAO CORP.
 PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
 XX WPI; 2004-328572/30.
 XX New alkaline protease having a mutant prepro sequence where amino acid
 PT residues at positions 52, 75 and 142 are substituted with another amino
 PT acid residue, useful as enzyme component of laundry detergents, or
 PT bleaching agents.
 XX Disclosure; SEQ ID NO 11; 29pp; English.
 XX The invention relates to an alkaline protease having a prepro sequence.
 CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
 CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
 CC acid residues at: (a) position 52 is substituted by aspartic acid or
 CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
 CC position 142 is substituted by lysine. The alkaline protease is useful as
 CC an enzyme which can be incorporated into laundry detergents, bleaching
 CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
 CC cleaning agents, and detergents for sterilising medical apparatus. The
 CC present sequence represents an alkaline protease used in homology

CC comparison with alkaline protease from *Bacillus* sp. KSM-KP43.

XX Sequence 434 AA;
 XX Query Match 99.8%; Score 2242; DB 8; Length 434;
 XX Best Local Similarity 99.8%; Pred. No. 1.5e-158;
 XX Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
 Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIQMDSGGGLGGLPSNLQTLFSQAYS 120
 Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIQMDSGGGLGGLPSNLQTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180
 Db 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240
 Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKGITPKPSLLKAAIAGAADIGLY 300
 Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKGITPKPSLLKAAIAGAADIGLY 300

Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
 Db 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

Qy 361 SVTLVNDLVLVITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
 Db 361 SVTLVNDLVLVITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGPQTFSLAIVN 434
 Db 421 VPVGPQTFSLAIVN 434

RESULT 13

ADSL4441
 ID ADS14441 standard; protein; 434 AA.

XX AC ADS14441;

XX 30-DEC-2004 (first entry)

XX *Bacillus* alkaline protease KP43 N187S mutant.

XX protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
 KW mutein.

XX *Bacillus* sp.; KSM-KP43.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 187 /note= "Wild-type Asn substituted by Ser"

XX EP1466962-A1.

XX 13-OCT-2004.

XX 08-APR-2004; 2004EP-00008504.

XX 10-APR-2003; 2003JP-00106709.

XX (KAOS) KAO CORP.

XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;

XX

DR WPI; 2004-711313/70.

XX New engineered alkaline protease, useful particularly in laundry
 PT detergents, comprising specified amino acids at particular positions.

XX Example 1; Page; 31pp; English.

XX The invention relates to a novel alkaline protease. The new alkaline
 CC protease comprises an amino acid sequence in which one or more amino acid
 CC residues selected from those located at 7 specific positions within
 CC ADS14427, or at positions corresponding to these positions are: position
 CC 15 (histidine), position 16 (threonine or glutamine), position 166
 CC (glycine), position 167 (valine), position 187 (serine), position 346
 CC (arginine), and position 405 (aspartic acid). The alkaline protease is
 CC useful in industry particularly in laundry detergents, but also e.g. in
 CC fibre modifying agents, leather processing agents, cosmetic compositions,
 CC bath additives, food-modifying agents, and pharmaceuticals. The present
 CC sequence represents an alkaline protease variant of the invention. Note:
 CC The present sequence is not represented in the specification, but has
 CC been created by the indexer using sequence shown in ADS14427 and
 CC information given in Example 1.

XX Sequence 434 AA;

Query Match 99.8%; Score 2242; DB 8; Length 434;

Best Local Similarity 99.8%; Pred. No. 1.5e-158;

Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIQMDSGGGLGGLPSNLQTLFSQAYS 120

Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIQMDSGGGLGGLPSNLQTLFSQAYS 120

Qy 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Db 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTTISAPGTAKNAI 180

Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240

Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240

Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKGITPKPSLLKAAIAGAADIGLY 300

Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVNKGITPKPSLLKAAIAGAADIGLY 300

Qy 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

Db 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

Qy 361 SVTLVNDLVLVITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Db 361 SVTLVNDLVLVITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420

Qy 421 VPVGPQTFSLAIVN 434

Db 421 VPVGPQTFSLAIVN 434

RESULT 14

AAV17091

ID AAV17091 standard; protein; 640 AA.

XX AAV17091;

XX 20-MAR-2003 (revised)

DT 21-JUL-1999 (first entry)

XX *Bacillus* alkaline protease.

XX Alkaline protease; *Bacillus*; casein digestion; oleic acid; enzyme;

Db	61	NANDTNGHGT	HVAGSVL	NGSTNKG	MAPQANL	VFQSIM	DGGGLG	LPNLQTL	FSQAYS	120
Qy	121	AGARIHTNS	KCAAVNG	AYTTDS	RNVDDY	VRKND	MTILFA	AGNE	PGNGTT	180
Db	121	AGARIHTNS	KCAAVNG	AYTTDS	RNVDDY	VRKND	MTILFA	AGNE	PGNGTT	180
Qy	181	TVGATENLR	PFSGSY	ADNINH	VAQFSS	RGPTK	DGR	IKPDV	MAPGTF	240
Db	181	TVGATENLR	PFSGSY	ADNINH	VAQFSS	RGPTK	DGR	IKPDV	MAPGTF	240
Qy	241	WANHDSKY	AYMG	GTSMAT	PIVAG	NVAQL	REH	FVN	RGIITPK	300
Db	241	WANHDSKY	AYMG	GTSMAT	PIVAG	NVAQL	REH	FVN	RGIITPK	300
Qy	301	PNGNQGW	RVTL	DKSL	NVAV	YN	ESSLS	TSQ	KATYS	360
Db	301	PNGNQGW	RVTL	DKSL	NVAV	YN	ESSLS	TSQ	KATYS	360
Qy	361	SVTLVND	LDLVIT	APNCTQ	VYVGN	DFTSP	YND	NMD	GRNN	420
Db	361	SVTLVND	LDLVIT	APNCTQ	VYVGN	DFTSP	YND	NMD	GRNN	420
Qy	421	VPVGPQT	FSLAIVN	434						
Db	421	VPVGPQT	FSLAIVN	434						

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